

TABLE 1: Included Genes

Lysine biosynthesis

| Nucleic Acid SEQ ID NO | Amino Acid SEQ ID NO | Identification Code | Contig. | NT Start | NT Stop | Function |
|---------------------------|-------------------------|---------------------|---------|----------|---------|---|
| 5 | 6 | RXA00657 | | | | AMINOACID BIOSYNTHESIS REGULATOR |
| 7 | 8 | RXA02229 | GR00653 | 2793 | 3617 | DIAMINOPELMATE EPIMERASE (EC 5.1.1.7) |
| 9 | 10 | RXS02970 | | | | ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11) |
| 11 | 12 | F RXA01009 | GR00287 | 4714 | 5943 | ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11) |
| 13 | 14 | RXC02390 | | | | MEMBRANE SPANNING PROTEIN INVOLVED IN LYSINE METABOLISM |
| 15 | 16 | RXC01796 | | | | MEMBRANE ASSOCIATED PROTEIN INVOLVED IN LYSINE METABOLISM |
| 17 | 18 | RXC01207 | | | | CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF LYSINE AND THREONINE |
| 19 | 20 | RXC00657 | | | | TRANSCRIPTIONAL REGULATOR INVOLVED IN LYSINE METABOLISM |
| 21 | 22 | RXC00552 | | | | CYTOSOLIC PROTEIN INVOLVED IN LYSINE METABOLISM |

Lysine biosynthesis

| Nucleic Acid SEQ ID NO | Amino Acid SEQ ID NO | Identification Code | Contig. | NT Start | NT Stop | Function |
|---------------------------|-------------------------|---------------------|---------|----------|---------|--|
| 23 | 24 | RXA00534 | GR00137 | 4758 | 3496 | ASPARTOKINASE ALPHA AND BETA SUBUNITS (EC 2.7.2.4) |
| 25 | 26 | RXA00533 | GR00137 | 3469 | 2438 | ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (EC 1.2.1.11) |
| 27 | 28 | RXA02843 | GR00842 | 543 | 4 | 2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117) |
| 29 | 30 | RXA02022 | GR00613 | 2063 | 3169 | SUCCINYL-DIAMINOPELMATE DESUCCINYLASE (EC 3.5.1.18) |
| 31 | 32 | RXA00044 | GR00007 | 3458 | 4393 | DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52) |
| 33 | 34 | RXA00863 | GR00236 | 896 | 1639 | DIHYDRODIPICOLINATE REDUCTASE (EC 1.3.1.26) |
| 35 | 36 | RXA00864 | GR00236 | 1694 | 2443 | probable 2,3-dihydrodipicolinate N-C6-lyase (cyclizing) (EC 4.3.3.-) - Corynebacterium glutamicum |
| 37 | 38 | RXA02843 | GR00842 | 543 | 4 | 2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117) |
| 39 | 40 | RXN00355 | VV0135 | 31980 | 30961 | MESO-DIAMINOPELMATE D-DEHYDROGENASE |
| 41 | 42 | F RXA00352 | GR00068 | 861 | 4 | MESO-DIAMINOPELMATE D-DEHYDROGENASE (EC 1.4.1.16) |
| 43 | 44 | RXA00972 | GR00274 | 3 | 1379 | DIAMINOPELMATE DECARBOXYLASE (EC 4.1.1.20) |
| 45 | 46 | RXA02653 | GR00752 | 5237 | 7234 | DIAMINOPELMATE DECARBOXYLASE (EC 4.1.1.20) |
| 47 | 48 | RXA01393 | GR00408 | 4249 | 3380 | LYSINE EXPORT REGULATOR PROTEIN |
| 49 | 50 | RXA00241 | GR00036 | 5443 | 6945 | L-LYSINE TRANSPORT PROTEIN |
| 51 | 52 | RXA01394 | GR00408 | 4320 | 5018 | LYSINE EXPORTER PROTEIN |
| 53 | 54 | RXA00865 | GR00236 | 2647 | 3549 | DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52) |

| Nucleic Acid SEQ ID NO | Amino Acid SEQ ID NO | Identification Code | Contig. | NT Start | NT Stop | Function |
|---------------------------|-------------------------|---------------------|---------|----------|---------|--|
| 55 | 56 | RXS02021 | | | | 2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117) |
| 57 | 58 | RXS02157 | | | | ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11) |
| 59 | 60 | RXC00733 | | | | ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM |
| 61 | 62 | RXC00861 | | | | PROTEIN INVOLVED IN LYSINE METABOLISM |
| 63 | 64 | RXC00866 | | | | ZN-DEPENDENT HYDROLASE INVOLVED IN LYSINE METABOLISM |
| 65 | 66 | RXC02095 | | | | ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM |
| 67 | 68 | RXC03185 | | | | PROTEIN INVOLVED IN LYSINE METABOLISM |

Metabolism of methionine and S-adenosyl methionine

| Nucleic Acid SEQ ID NO | Amino Acid SEQ ID NO | Identification Code | Contig. | NT Start | NT Stop | Function |
|---------------------------|-------------------------|---------------------|---------|----------|---------|---|
| 1 | 2 | metZ or met | | | | O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) |
| 3 | 4 | metC | | | | Cystathionine-γ-lyase |
| 69 | 70 | RXA00115 | GR00017 | 5359 | 4313 | HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.31) |
| 71 | 72 | RXN00403 | VV00086 | 70041 | 68911 | HOMOSERINE O-ACETYLTRANSFERASE |
| 73 | 74 | F RXA00403 | GR00088 | 723 | 1832 | HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.11) |
| 75 | 76 | RXS03158 | | | | CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9) |
| 77 | 78 | F RXA00254 | GR00038 | 2404 | 1811 | CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9) |
| 79 | 80 | RXA02532 | GR00726 | 3085 | 2039 | CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9) |
| 81 | 82 | RXS03159 | | | | CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9) |
| 83 | 84 | F RXA02768 | GR00770 | 1919 | 2521 | CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9) |
| 85 | 86 | RXA00216 | GR00032 | 16286 | 15297 | 5-methyltetrahydrofolate-homocysteine methyltransferase (methionine synthetase) |
| 87 | 94 | RXA02197 | GR00645 | 4552 | 4025 | 5-METHYLTETRAHYDROFOLATE-HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13) |
| 89 | 90 | RXN02198 | VV0302 | 9228 | 11726 | 5-METHYLTETRAHYDROFOLATE-HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13) |
| 91 | 91 | F RXA02198 | GR00646 | 2483 | 6 | 5-METHYLTETRAHYDROFOLATE-HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13) |
| 93 | 94 | RXN03074 | VV0042 | 2238 | 1741 | S-ADENOSYLMETHIONINE:2-DEMETHYLMENAUQUINONE METHYLTRANSFERASE (EC 2.1.-.-) |

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| <u>Nucleic Acid SEQ ID NO</u> | <u>Amino Acid SEQ ID NO</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|-----------------------------------|---------------------------------|----------------------------|----------------|-----------------|----------------|--|
| 95 | 96 | F RXA02906 | GR10044 | 1142 | 645 | S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.-) |
| 97 | 98 | RXN00132 | VW0124 | 3612 | 5045 | ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.-) |
| 99 | 100 | F RXA00132 | GR00020 | 7728 | 7624 | ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.-) |
| 101 | 102 | F RXA01371 | GR00398 | 2339 | 3634 | ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.-) |
| 103 | 104 | RXN02085 | | | | ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.-) |
| 105 | 106 | F RXA02085 | GR00629 | 3496 | 5295 | ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.-) |
| 107 | 108 | F RXA02086 | GR00629 | 5252 | 5731 | ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.-) |
| 109 | 110 | RXN02648 | | | | ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.-) |
| 111 | 112 | F RXA02648 | GR00751 | 5254 | 4730 | ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.-) |
| 113 | 114 | F RXA02658 | GR00752 | 14764 | 15447 | ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.-) |
| 115 | 116 | RXC02238 | | | | ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.-) |
| 117 | 118 | RXC00128 | | | | ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.1.-) |

S-2adenosyl methionine (SAM) Biosynthesis

| <u>Nucleic Acid SEQ ID NO</u> | <u>Amino Acid SEQ ID NO</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|-----------------------------------|---------------------------------|----------------------------|----------------|-----------------|----------------|--|
| 119 | 120 | RXA02240 | GR00654 | 7160 | 8380 | S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) |

TABLE 2: GENES IDENTIFIED FROM GENBANK

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|---|------------------|--|--|
| A09073 | ppg | Phosphoenol pyruvate carboxylase | Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-amino acids using said strains," Patent: EP 0358940-A 3 03/21/90 |
| A45579, A45581, A45583, A45585 A45587 | | Threonine dehydratase | Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95 |
| AB003132 | murC; ftsQ; ftsZ | | Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997) |
| AB015023 | murC; ftsQ | | Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999) |
| AB018530 | ftsR | | Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996) |
| AB018531 | ftsR1; ftsR2 | | |
| AB020624 | murI | D-glutamate racemase | |
| AB023377 | tkt | transketolase | |
| AB024708 | gltB; gltD | Glutamine 2-oxoglutarate aminotransferase large and small subunits | |
| AB025424 | acn | aconitase | |
| AB027714 | rep | Replication protein | |
| AB027715 | rep; aad | Replication protein; aminoglycoside adenylyltransferase | |
| AF005242 | argC | N-acetylglutamate-5-semialdehyde dehydrogenase | |
| AF005635 | glnA | Glutamine synthetase | |
| AF030405 | hisF | cyclase | |
| AF030520 | argG | Argininosuccinate synthetase | |
| AF031518 | argF | Ornithine carbamoyltransferase | |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|------------------------|--|---|---|
| AF036932 | aroD | 3-dehydroquinate dehydratase | |
| AF038548 | pyc | Pyruvate carboxylase | |
| AF038651 | dcIAE; apt; rel | Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase | Wehmeier, L. et al. "The role of the <i>Corynebacterium glutamicum</i> rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998) |
| AF041436 | argR | Arginine repressor | |
| AF045998 | impA | Inositol monophosphate phosphatase | |
| AF048764 | argH | Argininosuccinate lyase | |
| AF049897 | argC; argJ; argB; argD; argF; argR; argG; argH | N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase | |
| AF050109 | inhA | Enoyl-acyl carrier protein reductase | |
| AF050166 | hisG | ATP phosphoribosyltransferase | |
| AF051846 | hisA | Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase | |
| AF052652 | metA | Homoserine O-acetyltransferase | Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in <i>Corynebacterium glutamicum</i> ," <i>Mol. Cells</i> , 8(3):286-294 (1998) |
| AF053071 | aroB | Dehydroquinate synthetase | |
| AF060558 | hisH | Glutamine amidotransferase | |
| AF086704 | hisE | Phosphoribosyl-ATP-pyrophosphohydrolase | |
| AF114233 | aroA | 5-enolpyruvylshikimate 3-phosphate synthase | |
| AF116184 | panD | L-aspartate-alpha-decarboxylase precursor | Dusch, N. et al. "Expression of the <i>Corynebacterium glutamicum</i> panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in <i>Escherichia coli</i> ," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|------------------------|-----------------------------|---|--|
| AF124518 | aroD; aroE | 3-dehydroquinase; shikimate dehydrogenase | |
| AF124600 | aroC; aroK; aroB; pepQ | Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase | |
| AF145897 | inhA | | |
| AF145898 | inhA | | |
| AJ001436 | ectP | Transport of ectoine, glycine betaine, proline | Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998) |
| AJ004934 | dapD | Tetrahydrodipicolinate succinylase (incomplete) | Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998) |
| AJ007732 | ppc; secG; amt; ocd; soxA | Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase | |
| AJ010319 | ftsY; glnB; glnD; srp; amtP | Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein | Jakoby, M. et al. "Nitrogen regulation in Corynebacterium glutamicum; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEBS Microbiol.</i> , 173(2):303-310 (1999) |
| AJ132968 | cat | Chloramphenicol acetyl transferase | |
| AJ224946 | mgo | L-malate: quinone oxidoreductase | Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from Corynebacterium glutamicum," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998) |
| AJ238250 | ndh | NADH dehydrogenase | |
| AJ238703 | porA | Porin | Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of Corynebacterium glutamicum: The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998) |
| D17429 | | Transposable element IS31831 | Vertes et al. "Isolation and characterization of IS31831, a transposable element from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|--|-----------|--|---|
| E05112 | | Dihydro-dipichorinate synthetase | Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93 |
| E05776 | | Diaminopimelic acid dehydrogenase | Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93 |
| E05779 | | Threonine synthase | Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93 |
| E06110 | | Prephenate dehydratase | Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93 |
| E06111 | | Mutated Prephenate dehydratase | Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93 |
| E06146 | | Acetohydroxy acid synthetase | Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93 |
| E06825 | | Aspartokinase | Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94 |
| E06826 | | Mutated aspartokinase alpha subunit | Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94 |
| E06827 | | Mutated aspartokinase alpha subunit | Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94 |
| E07701 | secY | | Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94 |
| E08177 | | Aspartokinase | Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94 |
| E08178, E08179, E08180, E08181, E08182 | | Feedback inhibition-released Aspartokinase | Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94 |
| E08232 | | Acetohydroxy-acid isomerase | Inui, M. et al. "Gene DNA coding acetohydroxy acid isomerase," Patent: JP 1994277067-A 1 10/04/94 |
| E08234 | secE | | Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94 |
| E08643 | | FT aminotransferase and desthiobiotin synthetase promoter region | Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95 |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|------------------------------|------------------|--|---|
| E08646 | | Biotin synthetase | Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95 |
| E08649 | | Aspartase | Kohana, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95 |
| E08900 | | Dihydrodipicolinate reductase | Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95 |
| E08901 | | Diaminopimelic acid decarboxylase | Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95 |
| E12594 | | Serine hydroxymethyltransferase | Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97 |
| E12760, E12759, E12758 | | transposase | Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97 |
| E12764 | | Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase | Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97 |
| E12767 | | Dihydrodipicolinic acid synthetase | Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97 |
| E12770 | | aspartokinase | Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97 |
| E12773 | | Dihydrodipicolinic acid reductase | Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97 |
| E13655 | | Glucose-6-phosphate dehydrogenase | Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97 |
| L01508 | IlvA | Threonine dehydratase | Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992) |
| L07603 | EC 4.2.1.15 | 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase | Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993) |
| L09232 | IlvB; ilvN; ilvC | Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase | Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|------------------------|-----------|--|---|
| L18874 | PtsM | Phosphoenolpyruvate sugar phosphotransferase | Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in <i>Escherichia coli</i> and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994) |
| L27123 | aceB | Malate synthase | Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994) |
| L27126 | | Pyruvate kinase | Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994) |
| L28760 | aceA | Isocitrate lyase | Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," <i>J. Bacteriol.</i> , 177(2):465-467 (1995) |
| L35906 | dtxr | Diphtheria toxin repressor | Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986) |
| M13774 | | Prephenate dehydratase | Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 56 rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987) |
| M16175 | 5S rRNA | | Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987) |
| M16663 | trpE | Anthranilate synthase, 5' end | Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987) |
| M16664 | trpA | Tryptophan synthase, 3' end | Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987) |
| M25819 | | Phosphoenolpyruvate carboxylase | O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," <i>Gene</i> , 77(2):237-251 (1989) |
| M85106 | | 23S rRNA gene insertion sequence | Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|------------------------|-----------------------|--|---|
| M85107, M85108 | | 23S rRNA gene insertion sequence | Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992) |
| M89931 | aecD; brnQ; yhbW | Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW | Rosol, I. et al. "The Corynebacterium glutamicum aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminothylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998) |
| S59299 | trp | Leader gene (promoter) | Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993) |
| U11545 | trpD | Anthranyl phosphate transferase | O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland. |
| U13922 | cgIIIM; cgIIR; clgIIR | Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease | Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cgIIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," <i>Gene</i> , 203(2):95-101 (1997) |
| U14965 | recA | | |
| U31224 | ppx | | Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996) |
| U31225 | proC | L-proline: NADP+ 5-oxidoreductase | Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996) |
| U31230 | obg; proB; unkdh | ?; gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases | Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|---------------------------|--|--|---|
| U31281 | bioB | Biotin synthase | Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996) |
| U35023 | thiR; accBC | Thiosulfate sulfurtransferase; acyl CoA carboxylase | Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996) |
| U43535 | cmr | Multidrug resistance protein | Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997) |
| U43536 | clpB | Heat shock A TP-binding protein | |
| U53587 | aphA-3 | 3'5"-aminoglycoside phosphotransferase | |
| U89648 | | <i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence | |
| X04960 | trpA; trpB; trpC; trpD; trpE; trpG; trpL | Tryptophan operon | Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986) |
| X07563 | lys A | DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20) | Yeh, P. et al. "Nucleic sequence of the <i>lysA</i> gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988) |
| X14234 | EC 4.1.1.31 | Phosphoenolpyruvate carboxylase | Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993) |
| X17313 | fda | Fructose-bisphosphate aldolase | Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i> |
| X53993 | dapA | L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52) | Bonnassie, S. et al. "Nucleic sequence of the <i>dapA</i> gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|---------------------------|----------------------------|--|---|
| X54223 | | AttB-related site | Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambdacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990) |
| X54740 | argS; lysA | Arginyl-tRNA synthetase; Diaminopimelate decarboxylase | Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990) |
| X55994 | trpL; trpE | Putative leader peptide; anthranilate synthase component 1 | Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990) |
| X56037 | thrC | Threonine synthase | Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990) |
| X56075 | attB-related site | Attachment site | Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambdacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990) |
| X57226 | lysC-alpha; lysC-beta; asd | Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase | Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990) |
| X59403 | gap;pgk; tpi | Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase | Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992) |
| X59404 | gdh | Glutamate dehydrogenase | Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992) |
| X60312 | lysI | L-lysine permease | Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|------------------------|------------|----------------------------------|---|
| X66078 | copI | PsI protein | Joliff, G. et al. "Cloning and nucleotide sequence of the cspI gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992) |
| X66112 | glt | Citrate synthase | Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994) |
| X67737 | dapB | Dihydrodipicolinate reductase | Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993) |
| X69103 | csp2 | Surface layer protein PS2 | Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994) |
| X69104 | | IS3 related insertion element | Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994) |
| X70959 | leuA | Isopropylmalate synthase | Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995) |
| X71489 | icd | Isocitrate dehydrogenase (NADP+) | |
| X72855 | GDHA | Glutamate dehydrogenase (NADP+) | Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994) |
| X75083, X70584 | mttA | 5-methyltryptophan resistance | Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994) |
| X75085 | recA | | |
| X75504 | aceA; thiX | Partial Isocitrate lyase; ? | Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994) |
| X76875 | | ATPase beta-subunit | Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|------------------------|------------------------|---|--|
| X77034 | tuf | Elongation factor Tu | Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993) |
| X77384 | recA | | Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994) |
| X78491 | aceB | Malate synthase | Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994) |
| X80629 | 16S rDNA | 16S ribosomal RNA | Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995) |
| X81191 | gluA; gluB; gluC; gluD | Glutamate uptake system | Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995) |
| X81379 | dapE | Succinylidiaminopimelate desuccinylase | Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994) |
| X82061 | 16S rDNA | 16S ribosomal RNA | Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995) |
| X82928 | asd; lysC | Aspartate-semialdehyde dehydrogenase; ? | Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995) |
| X82929 | proA | Gamma-glutamyl phosphate reductase | Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995) |
| X84257 | 16S rDNA | 16S ribosomal RNA | Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995) |
| X85965 | aroP; dapE | Aromatic amino acid permease; ? | Wehrmann et al. "Functional analysis of sequences adjacent to dapE of <i>C. glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|---------------------------|---------------------------------|---|---|
| X86157 | argB; argC; argD; argF; argJ | Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase | Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996) |
| X89084 | pta; ackA | Phosphate acetyltransferase; acetate kinase | Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999) |
| X89850 | attB | Attachment site | Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting 'Arthrobacter aureus C70,' <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996) |
| X90356 | | Promoter fragment F1 | Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90357 | | Promoter fragment F2 | Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90358 | | Promoter fragment F10 | Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90359 | | Promoter fragment F13 | Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90360 | | Promoter fragment F22 | Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90361 | | Promoter fragment F34 | Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90362 | | Promoter fragment F37 | Patek, M. et al. "Promoters from <i>C. glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|---------------------------|------------------|---|---|
| X90363 | | Promoter fragment F45 | Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90364 | | Promoter fragment F64 | Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90365 | | Promoter fragment F75 | Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90366 | | Promoter fragment PF101 | Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90367 | | Promoter fragment PF104 | Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90368 | | Promoter fragment PF109 | Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X93513 | amt | Ammonium transport system | Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996) |
| X93514 | betP | Glycine betaine transport system | Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996) |
| X95649 | orf4 | | Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997) |
| X96471 | lysE; lysG | Lysine exporter protein; Lysine export regulator protein | Vrjlic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996) |
| X96580 | panB; panC; xylB | 3-methyl-2-oxobutanate hydroxymethyltransferase; pantoate-beta- | Sahm, H. et al. "D-pantothenate synthesis in <i>Corynebacterium glutamicum</i> and use of panBC and genes encoding L-valine synthesis for D-pantothenate |

| GenBank™ Accession No. | Gene Name | alanine ligase; xylulokinase Gene Function | overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999) Reference |
|---------------------------|-----------------------|--|--|
| X96962 | | Insertion sequence IS1207 and transposase | |
| X99289 | | Elongation factor P | Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer <i>Brevibacterium lactofermentum</i> (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997) |
| Y00140 | thrB | Homoserine kinase | Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987) |
| Y00151 | ddh | Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16) | Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987) |
| Y00476 | thrA | Homoserine dehydrogenase | Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987) |
| Y00546 | hom; thrB | Homoserine dehydrogenase; homoserine kinase | Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the <i>Corynebacterium glutamicum</i> hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988) |
| Y08964 | mutC; ftsQ/divD; ftsZ | UPD-N-acetylmutamate-alanine ligase; division initiation protein or cell division protein; cell division protein | Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from <i>Brevibacterium lactofermentum</i> ," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998) |
| Y09163 | putP | High affinity proline transport system | Peter, H. et al. "Isolation of the putP gene of <i>Corynebacterium glutamicum</i> proline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997) |
| Y09548 | pyc | Pyruvate carboxylase | Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from <i>Corynebacterium glutamicum</i> : characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998) |
| Y09578 | leuB | 3-isopropylmalate dehydrogenase | Patek, M. et al. "Analysis of the leuB gene from <i>Corynebacterium glutamicum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998) |
| Y12472 | | Attachment site bacteriophage Phi-16 | Moreau, S. et al. "Site-specific integration of corynephage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999) |
| Y12537 | proP | Proline/ectoine uptake system protein | Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|------------------------|------------|--|--|
| Y13221 | glnA | Glutamine synthetase I | Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997) |
| Y16642 | lpd | Dihydrolipoamide dehydrogenase | Moreau, S. et al. "Analysis of the integration functions of φ304L: An inte-grase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999) |
| Y18059 | | Attachment site Corynephage 304L | |
| Z21501 | argS; lysA | Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial) | Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993) |
| Z21502 | dapA; dapB | Dihydrodipicolinate synthase; dihydrodipicolinate reductase | Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993) |
| Z29563 | thrC | Threonine synthase | Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994) |
| Z46753 | 16S rDNA | Gene for 16S ribosomal RNA | |
| Z49822 | sigA | SigA sigma factor | Oguiza, J.A. et al "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996) |
| Z49823 | galE; dtxR | Catalytic activity UDP-galactose 4-epimerase; diptheria toxin regulatory protein | Oguiza, J.A. et al "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996) |
| Z49824 | orf1; sigB | ?; SigB sigma factor | Oguiza, J.A. et al "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996) |
| Z66534 | | Transposase | Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996) |

A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

| Genus | species | ATCC | FERM | NRRL | CECT | NCIMB | CBS | NCTC | DSMZ |
|----------------|----------------|-------|------|--------|------|-------|-----|------|------|
| Brevibacterium | ammoniagenes | 21054 | | | | | | | |
| Brevibacterium | ammoniagenes | 19350 | | | | | | | |
| Brevibacterium | ammoniagenes | 19351 | | | | | | | |
| Brevibacterium | ammoniagenes | 19352 | | | | | | | |
| Brevibacterium | ammoniagenes | 19353 | | | | | | | |
| Brevibacterium | ammoniagenes | 19354 | | | | | | | |
| Brevibacterium | ammoniagenes | 19355 | | | | | | | |
| Brevibacterium | ammoniagenes | 19356 | | | | | | | |
| Brevibacterium | ammoniagenes | 21055 | | | | | | | |
| Brevibacterium | ammoniagenes | 21077 | | | | | | | |
| Brevibacterium | ammoniagenes | 21553 | | | | | | | |
| Brevibacterium | ammoniagenes | 21580 | | | | | | | |
| Brevibacterium | ammoniagenes | 39101 | | | | | | | |
| Brevibacterium | butanicum | 21196 | | | | | | | |
| Brevibacterium | divaricatum | 21792 | P928 | | | | | | |
| Brevibacterium | flavum | 21474 | | | | | | | |
| Brevibacterium | flavum | 21129 | | | | | | | |
| Brevibacterium | flavum | 21518 | | | | | | | |
| Brevibacterium | flavum | | | B11474 | | | | | |
| Brevibacterium | flavum | | | B11472 | | | | | |
| Brevibacterium | flavum | 21127 | | | | | | | |
| Brevibacterium | flavum | 21128 | | | | | | | |
| Brevibacterium | flavum | 21427 | | | | | | | |
| Brevibacterium | flavum | 21475 | | | | | | | |
| Brevibacterium | flavum | 21517 | | | | | | | |
| Brevibacterium | flavum | 21528 | | | | | | | |
| Brevibacterium | flavum | 21529 | | | | | | | |
| Brevibacterium | flavum | | | B11477 | | | | | |
| Brevibacterium | flavum | | | B11478 | | | | | |
| Brevibacterium | flavum | 21127 | | | | | | | |
| Brevibacterium | flavum | | | B11474 | | | | | |
| Brevibacterium | healii | 15527 | | | | | | | |
| Brevibacterium | ketoglutamicum | 21004 | | | | | | | |
| Brevibacterium | ketoglutamicum | 21089 | | | | | | | |
| Brevibacterium | ketosoreductum | 21914 | | | | | | | |
| Brevibacterium | lactofermentum | | | | 70 | | | | |
| Brevibacterium | lactofermentum | | | | 74 | | | | |
| Brevibacterium | lactofermentum | | | | 77 | | | | |
| Brevibacterium | lactofermentum | 21798 | | | | | | | |
| Brevibacterium | lactofermentum | 21799 | | | | | | | |
| Brevibacterium | lactofermentum | 21800 | | | | | | | |
| Brevibacterium | lactofermentum | 21801 | | | | | | | |
| Brevibacterium | lactofermentum | | | B11470 | | | | | |
| Brevibacterium | lactofermentum | | | B11471 | | | | | |

| Genus | species | ATCC | FERM | NRRL | CECT | NCIMB | CBS | NCTC | DSMZ |
|-----------------|------------------|-------|------|--------|------|-------|--------|------|------|
| Brevibacterium | lactofermentum | 21086 | | | | | | | |
| Brevibacterium | lactofermentum | 21420 | | | | | | | |
| Brevibacterium | lactofermentum | 21086 | | | | | | | |
| Brevibacterium | lactofermentum | 31269 | | | | | | | |
| Brevibacterium | linens | 9174 | | | | | | | |
| Brevibacterium | linens | 19391 | | | | | | | |
| Brevibacterium | linens | 8377 | | | | | | | |
| Brevibacterium | paraffinolyticum | | | | | 11160 | | | |
| Brevibacterium | spec. | | | | | | 717.73 | | |
| Brevibacterium | spec. | | | | | | 717.73 | | |
| Brevibacterium | spec. | 14604 | | | | | | | |
| Brevibacterium | spec. | 21860 | | | | | | | |
| Brevibacterium | spec. | 21864 | | | | | | | |
| Brevibacterium | spec. | 21865 | | | | | | | |
| Brevibacterium | spec. | 21866 | | | | | | | |
| Brevibacterium | spec. | 19240 | | | | | | | |
| Corynebacterium | acetoacidophilum | 21476 | | | | | | | |
| Corynebacterium | acetoacidophilum | 13870 | | | | | | | |
| Corynebacterium | acetoglutamicum | | | B11473 | | | | | |
| Corynebacterium | acetoglutamicum | | | B11475 | | | | | |
| Corynebacterium | acetoglutamicum | 15806 | | | | | | | |
| Corynebacterium | acetoglutamicum | 21491 | | | | | | | |
| Corynebacterium | acetoglutamicum | 31270 | | | | | | | |
| Corynebacterium | acetophilum | | | B3671 | | | | | |
| Corynebacterium | ammoniagenes | 6872 | | | | | | 2399 | |
| Corynebacterium | ammoniagenes | 15511 | | | | | | | |
| Corynebacterium | fujikense | 21496 | | | | | | | |
| Corynebacterium | glutamicum | 14067 | | | | | | | |
| Corynebacterium | glutamicum | 39137 | | | | | | | |
| Corynebacterium | glutamicum | 21254 | | | | | | | |
| Corynebacterium | glutamicum | 21255 | | | | | | | |
| Corynebacterium | glutamicum | 31830 | | | | | | | |
| Corynebacterium | glutamicum | 13032 | | | | | | | |
| Corynebacterium | glutamicum | 14305 | | | | | | | |
| Corynebacterium | glutamicum | 15455 | | | | | | | |
| Corynebacterium | glutamicum | 13058 | | | | | | | |
| Corynebacterium | glutamicum | 13059 | | | | | | | |
| Corynebacterium | glutamicum | 13060 | | | | | | | |
| Corynebacterium | glutamicum | 21492 | | | | | | | |
| Corynebacterium | glutamicum | 21513 | | | | | | | |
| Corynebacterium | glutamicum | 21526 | | | | | | | |
| Corynebacterium | glutamicum | 21543 | | | | | | | |
| Corynebacterium | glutamicum | 13287 | | | | | | | |
| Corynebacterium | glutamicum | 21851 | | | | | | | |
| Corynebacterium | glutamicum | 21253 | | | | | | | |
| Corynebacterium | glutamicum | 21514 | | | | | | | |
| Corynebacterium | glutamicum | 21516 | | | | | | | |
| Corynebacterium | glutamicum | 21299 | | | | | | | |

| Genus | species | ATCC | FERM | NRRL | CECT | NCIMB | CBS | NCTC | DSMZ | Other origin |
|-----------------|----------------|-------|-------|--------|------|-------|-----|------|-------|--------------|
| Corynebacterium | glutamicum | | | B12418 | | | | | | |
| Corynebacterium | glutamicum | | | B11476 | | | | | | |
| Corynebacterium | glutamicum | 21608 | | | | | | | | |
| Corynebacterium | lilium | | P973 | | | | | | | |
| Corynebacterium | nitrilophilus | 21419 | | | | 11594 | | | | |
| Corynebacterium | spec. | | P4445 | | | | | | | |
| Corynebacterium | spec. | | P4446 | | | | | | | |
| Corynebacterium | spec. | 31088 | | | | | | | | |
| Corynebacterium | spec. | 31089 | | | | | | | | |
| Corynebacterium | spec. | 31090 | | | | | | | | |
| Corynebacterium | spec. | 31090 | | | | | | | | |
| Corynebacterium | spec. | 31090 | | | | | | | | |
| Corynebacterium | spec. | 15954 | | | | | | | 20145 | |
| Corynebacterium | spec. | 21857 | | | | | | | | |
| Corynebacterium | spec. | 21862 | | | | | | | | |
| Corynebacterium | spec. | 21863 | | | | | | | | |
| Corynebacterium | Glutamicum* | | | | | | | | | ASO19 |
| Corynebacterium | Glutamicum** | | | | | | | | | ASO19 E12 |
| Corynebacterium | Glutamicum*** | | | | | | | | | HL457 |
| Corynebacterium | Glutamicum**** | | | | | | | | | HL459 |

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japan.

* Spontaneous rifampin-resistant mutant of *C. glutamicum* ATCC13059^d Yoshihama et al., 1985

** Restriction-deficient variant of ASO19 Follett et al., 1993

*** *metC*-disrupted mutant of ASO19E12 This study

**** *metC*-disrupted mutant of ASO19E12 This study

TABLE 4: ALIGNMENT RESULTS

| ID # | length (NT) | Genbank Hit | Length | Accession | Name of Genbank Hit | Source of Genbank Hit | % homology (GAP) | Date of Deposit |
|---------|----------------|-------------------|--------|-----------|---|-----------------------------|---------------------|--------------------------------------|
| rx00657 | 906 | GB_BA1:AF064700 | 3481 | AF064700 | Rhodococcus sp NO1-1 CprS and CprR genes, complete cds. | Rhodococcus sp | 40,265 | 15-Jul-98 |
| metc | 1314 | GB_BA2:MTV016 | 53862 | AL021841 | Mycobacterium tuberculosis H37Rv complete genome, segment 143/162 | Mycobacterium tuberculosis | 61,278 | 23-Jun-99 |
| metc | 978 | GB_BA2:CORCSLYS | 2821 | M89831 | Corynebacterium glutamicum beta C-S lyase (aecD) and branched-chain amino acid uptake | Corynebacterium glutamicum | 99,591 | 04-JUN-1998 |
| rx00023 | 3579 | GB_EST33:AI776129 | 483 | AI776129 | EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone | Lycopersicon esculentum | 40,956 | 29-Jun-99 |
| | | GB_EST33:AI776129 | 483 | AI776129 | clER17D3, mRNA sequence. | Lycopersicon esculentum | 40,956 | 29-Jun-99 |
| | | GB_EST33:AI776129 | 483 | AI776129 | EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone | Lycopersicon esculentum | 40,956 | 29-Jun-99 |
| | | GB_EST33:AI776129 | 483 | AI776129 | clER17D3, mRNA sequence. | Lycopersicon esculentum | 40,956 | 29-Jun-99 |
| rx00044 | 1059 | EM_PAT:E11760 | 6911 | E11760 | Base sequence of sucrose gene. | Corynebacterium glutamicum | 42,979 | 08-OCT-1997 (Rel. 52, Created) |
| | | GB_PAT:I26124 | 6911 | I26124 | Sequence 4 from patent US 5556776. | Unknown. | 42,979 | 07-OCT-1996 |
| | | GB_BA2:ECOUW89 | 176195 | U00006 | E. coli chromosomal region from 89.2 to 92.8 minutes. | Escherichia coli | 39,097 | 17-DEC-1993 |
| rx00064 | 1401 | GB_PAT:E16763 | 2517 | E16763 | gDNA encoding aspartate transferase (AAT). | Corynebacterium glutamicum | 95,429 | 28-Jul-99 |
| | | GB_HTG2:AC007892 | 134257 | AC007892 | Drosophila melanogaster chromosome 3 clone BACR02O03 (D797) RPCI-98 | Drosophila melanogaster | 31,111 | 2-Aug-99 |
| | | GB_HTG2:AC007892 | 134257 | AC007892 | 02.O.3 map 99B-99B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 113 unordered pieces. | Drosophila melanogaster | 31,111 | 2-Aug-99 |
| rx00072 | | GB_HTG2:AC007892 | 134257 | AC007892 | Drosophila melanogaster chromosome 3 clone BACR02O03 (D797) RPCI-98 02.O.3 map 99B-99B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 113 unordered pieces. | Drosophila melanogaster | 31,111 | 2-Aug-99 |
| rx00105 | 798 | GB_BA1:MTV002 | 56414 | AL008967 | Mycobacterium tuberculosis H37Rv complete genome; segment 122/162. | Mycobacterium tuberculosis | 37,753 | 17-Jun-98 |
| | | GB_BA1:ECU29581 | 71128 | U29581 | Escherichia coli K-12 genome; approximately 63 to 64 minutes. | Escherichia coli | 35,669 | 14-Jan-97 |
| | | GB_BA2:AE000366 | 10405 | AE000366 | Escherichia coli K-12 MG1655 section 256 of 400 of the complete genome. | Escherichia coli | 35,669 | 12-Nov-98 |
| rx00106 | 579 | GB_EST15:AA494237 | 367 | AA494237 | ng83f04.s1 NCI_CGAP_P16 Homo sapiens cDNA clone IMAGE:941407 similar to SW:DYR_LACCA P00381 DIHYDROFOLATE REDUCTASE ;, mRNA sequence. | Homo sapiens | 42,896 | 20-Aug-97 |
| | | GB_BA2:AF161327 | 2021 | AF161327 | Corynebacterium diphtheriae histidine kinase ChrS (chrS) and response regulator ChrA (chrA) genes, complete cds. | Corynebacterium diphtheriae | 40,210 | 9-Sep-99 |
| | | GB_PAT:AR041189 | 654 | AR041189 | Sequence 4 from patent US 5811286. | Unknown. | 41,176 | 29-Sep-99 |
| rx00115 | 1170 | GB_PR4:AC007110 | 148336 | AC007110 | Homo sapiens chromosome 17, clone hRPK.472_J_18, complete sequence. | Homo sapiens | 36,783 | 30-MAR-1999 |
| | | GB_HTG3:AC008537 | 170030 | AC008537 | Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING IN PROGRESS ***; 93 unordered pieces. | Homo sapiens | 40,296 | 2-Sep-99 |
| | | GB_HTG3:AC008537 | 170030 | AC008537 | Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING IN PROGRESS ***; 93 unordered pieces. | Homo sapiens | 40,296 | 2-Sep-99 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|-------------------|--------|----------|---|----------------------------------|--------|-------------|
| rx00116 | 1284 | GB_BA2:AF062345 | 16458 | AF062345 | Caulobacter crescentus Sst1 (sst1), S-layer protein subunit (rsaA), ABC transporter (rsaD), membrane forming unit (rsaE), putative GDP-mannose-4,6-dehydratase (lpsA), putative acetyltransferase (lpsB), putative perosamine synthetase (lpsC), putative mannose-6-phosphate isomerase (lpsD), putative mannose-6-phosphate isomerase (lpsE), outer membrane protein (rsaF), and putative perosamine transferase (lpsE) genes, complete cds. | Caulobacter crescentus | 36,235 | 19-OCT-1999 |
| | | GB_PAT:118647 | 3300 | I118647 | Sequence 6 from patent US 5500353. | Unknown. | 36,821 | 07-OCT-1996 |
| | | GB_GSS13:AQ446197 | 751 | AQ446197 | nbxb0062D16r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0062D16r, genomic survey sequence. | Oryza sativa | 38,124 | 8-Apr-99 |
| rx00131 | 732 | GB_BA1:MTY20B11 | 36330 | Z95121 | Mycobacterium tuberculosis H37Rv complete genome; segment 139/162. | Mycobacterium tuberculosis | 43,571 | 17-Jun-98 |
| | | GB_BA1:SAR7932 | 15176 | AJ007932 | Streptomyces argillaceus mithramycin biosynthetic genes. | Streptomyces argillaceus | 41,116 | 15-Jun-99 |
| | | GB_BA1:MTY20B11 | 36330 | Z95121 | Mycobacterium tuberculosis H37Rv complete genome; segment 139/162. | Mycobacterium tuberculosis | 39,726 | 17-Jun-98 |
| rx00132 | 1557 | GB_BA1:MTY20B11 | 36330 | Z95121 | Mycobacterium tuberculosis H37Rv complete genome; segment 139/162. | Mycobacterium tuberculosis | 36,788 | 17-Jun-98 |
| | | GB_IN2:TVU40872 | 1882 | U40872 | Trichomonas vaginalis S-adenosyl-L-homocysteine hydrolase gene, complete cds. | Trichomonas vaginalis | 61,914 | 31-OCT-1996 |
| | | GB_HTG6:AC010706 | 169265 | AC010706 | Drosophila melanogaster chromosome X clone BACR36D15 (D887) RPCI-98 36.D.15 map 13C-13E strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 74 unordered pieces. | Drosophila melanogaster | 51,325 | 22-Nov-99 |
| rx00145 | 1059 | GB_BA1:MTY2B12 | 20431 | Z81011 | Mycobacterium tuberculosis H37Rv complete genome; segment 61/162. | Mycobacterium tuberculosis | 63,365 | 18-Jun-98 |
| | | GB_BA1:PSEPVRBX | 2273 | L19649 | Pseudomonas aeruginosa aspartate transcarbamoylase (pyrB) and dihydroorotase-like (pyrX) genes, complete cds's. | Pseudomonas aeruginosa | 56,080 | 26-Jul-93 |
| | | GB_BA1:LLPYRBDNA | 1468 | X84262 | L. leichmannii pyrB gene. | Lactobacillus leichmannii | 47,514 | 29-Apr-97 |
| rx00146 | 1464 | GB_BA1:MTY2B12 | 20431 | Z81011 | Mycobacterium tuberculosis H37Rv complete genome; segment 61/162. | Mycobacterium tuberculosis | 60,714 | 18-Jun-98 |
| | | GB_BA1:MTY154 | 13935 | Z98209 | Mycobacterium tuberculosis H37Rv complete genome; segment 121/162. | Mycobacterium tuberculosis | 39,229 | 17-Jun-98 |
| | | GB_BA1:MSGY154 | 40221 | AD000002 | Mycobacterium tuberculosis sequence from clone y154. | Mycobacterium tuberculosis | 36,618 | 03-DEC-1996 |
| rx00147 | 1302 | GB_BA1:MTY2B12 | 20431 | Z81011 | Mycobacterium tuberculosis H37Rv complete genome; segment 61/162. | Mycobacterium tuberculosis | 61,527 | 18-Jun-98 |
| | | GB_BA1:MSGB937CS | 38914 | L78820 | Mycobacterium leprae cosmid B937 DNA sequence. | Mycobacterium leprae | 59,538 | 15-Jun-96 |
| | | GB_BA1:PAU81259 | 7285 | U81259 | Pseudomonas aeruginosa dihydrodipicolinate reductase (dapB) gene, partial cds, carbamoylphosphate synthetase small subunit (carA) and carbamoylphosphate synthetase large subunit (carB) genes, complete cds, and FtsJ homolog (ftsJ) gene, partial cds. | Pseudomonas aeruginosa | 55,396 | 23-DEC-1996 |
| rx00155 | 1233 | GB_BA1:SC9B10 | 33320 | AL009204 | Streptomyces coelicolor cosmid 9B10. | Streptomyces coelicolor | 52,666 | 10-Feb-99 |
| | | GB_BA2:AF002133 | 15437 | AF002133 | Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds. | Mycobacterium avium | 54,191 | 26-MAR-1998 |
| | | GB_BA1:D85417 | 7984 | D85417 | Propionibacterium freudenreichii hemY, hemH, hemB, hemX, hemR and hemL genes, complete cds. | Propionibacterium freudenreichii | 46,667 | 6-Feb-99 |
| rx00166 | 783 | GB_HTG3:AC008167 | 174223 | AC008167 | Homo sapiens clone NH017Z013, *** SEQUENCING IN PROGRESS ***; 7 unordered pieces. | Homo sapiens | 37,451 | 21-Aug-99 |
| | | GB_HTG3:AC008167 | 174223 | AC008167 | Homo sapiens clone NH017Z013, *** SEQUENCING IN PROGRESS ***; 7 unordered pieces. | Homo sapiens | 37,451 | 21-Aug-99 |
| | | GB_HTG4:AC010118 | 80605 | AC010118 | Drosophila melanogaster chromosome 3L62B1 clone RPCI98-10D15, *** SEQUENCING IN PROGRESS ***; 51 unordered pieces. | Drosophila melanogaster | 38,627 | 16-OCT-1999 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|--------------------|--------|----------|--|----------------------------|---------|--------------------------------|
| rx00198 | 672 | GB_BA1:AB024708 | 8734 | AB024708 | Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds. | Corynebacterium glutamicum | 92,113 | 13-MAR-1999 |
| | | GB_BA1:AB024708 | 8734 | AB024708 | Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds. | Corynebacterium glutamicum | 93,702 | 13-MAR-1999 |
| | | GB_EST24:AI232702 | 528 | AI232702 | EST229390 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone RKICF35 3' end, mRNA sequence. | Rattus sp | 34,221 | 31-Jan-99 |
| rx00216 | 1113 | GB_HTG2:HSDJ850E9 | 117353 | AL121758 | Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS ***, in unordered pieces. | Homo sapiens | 37,965 | 03-DEC-1999 |
| | | GB_HTG2:HSDJ850E9 | 117353 | AL121758 | Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS ***, in unordered pieces. | Homo sapiens | 37,965 | 03-DEC-1999 |
| | | GB_PR2:CNS01DSA | 159400 | AL121766 | Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-412H8 of RPC1-11 library from chromosome 14 of Homo sapiens (Human), complete sequence. | Homo sapiens | 38,796 | 11-Nov-99 |
| rx00219 | 1065 | GB_HTG2:AC005079_0 | 110000 | AC005079 | Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces. | Homo sapiens | 38,227 | 22-Nov-98 |
| | | GB_HTG2:AC005079_1 | 110000 | AC005079 | Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces. | Homo sapiens | 38,227 | 22-Nov-98 |
| | | GB_HTG2:AC005079_1 | 110000 | AC005079 | Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces. | Homo sapiens | 38,227 | 22-Nov-98 |
| rx00223 | 1212 | GB_BA1:PPEA3NIF | 19771 | X99694 | Plasmid pEA3 nitrogen fixation genes. | Enterobacter agglomerans | 48,826 | 2-Aug-96 |
| | | GB_BA2:AF128444 | 2477 | AF128444 | Rhodobacter capsulatus molybdenum cofactor biosynthetic gene cluster, partial sequence. | Rhodobacter capsulatus | 40,135 | 22-MAR-1999 |
| | | GB_HTG4:AC010111 | 138938 | AC010111 | Drosophila melanogaster chromosome 3L70C1 clone RPC188-9B18, *** SEQUENCING IN PROGRESS ***, 64 unordered pieces. | Drosophila melanogaster | 39,527 | 16-OCT-1999 |
| rx00229 | 803 | GB_BA2:AF124518 | 1758 | AF124518 | Corynebacterium glutamicum 3-dehydroquinase (aroD) and shikimate dehydrogenase (aroE) genes, complete cds. | Corynebacterium glutamicum | 98,237 | 18-MAY-1999 |
| | | GB_PR3:AC004593 | 150221 | AC004593 | Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence. | Homo sapiens | 36,616 | 18-Apr-98 |
| | | GB_HTG2:AC006907 | 188972 | AC006907 | Caenorhabditis elegans clone Y76B12, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces. | Caenorhabditis elegans | 37,095 | 26-Feb-99 |
| rx00241 | 1626 | GB_BA1:CGLYSI | 4232 | X60312 | C-glutamicum lysyl gene for L-lysine permease. | Corynebacterium glutamicum | 100,000 | 30-Jan-92 |
| | | GB_HTG1:PFMAL13P1 | 192581 | AL049180 | Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces. | Plasmodium falciparum | 34,947 | 11-Aug-99 |
| | | GB_HTG1:PFMAL13P1 | 192581 | AL049180 | Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces. | Plasmodium falciparum | 34,947 | 11-Aug-99 |
| rx00262 | 1197 | GB_IN2:EHU89655 | 3219 | U89655 | Entamoeba histolytica unconventional myosin IB mRNA, complete cds. | Entamoeba histolytica | 36,496 | 23-MAY-1997 |
| | | GB_IN2:EHU89655 | 3219 | U89655 | Entamoeba histolytica unconventional myosin IB mRNA, complete cds. | Entamoeba histolytica | 37,544 | 23-MAY-1997 |
| rx00266 | 531 | GB_RO:AF016190 | 2939 | AF016190 | Mus musculus connexin-36 (Cx36) gene, complete cds. | Mus musculus | 41,856 | 9-Feb-99 |
| | | EM_PAT:E09719 | 3505 | E09719 | DNA encoding precursor protein of alkaline cellulase. | Bacillus sp. | 34,741 | 08-OCT-1997 (Rel. 52, Created) |
| | | GB_PAT:E02133 | 3494 | E02133 | gDNA encoding alkaline cellulase. | Bacillus sp. | 34,741 | 29-Sep-97 |
| | | GB_IN1:CEUK0568 | 36912 | AF040663 | Caenorhabditis elegans cosmid K05F6. | Caenorhabditis elegans | 36,943 | 6-Jan-98 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | |
|-------------------|-------|----------|---|-------------------------------|---------|-------------|
| GB_BA1:CGU43535 | 2531 | U43535 | Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds. | Corynebacterium glutamicum | 36,658 | 9-Apr-97 |
| GB_RO:RNU30789 | 3510 | U30789 | Rattus norvegicus clone N27 mRNA. | Rattus norvegicus | 38,190 | 20-Aug-96 |
| GB_BA2:CGU31281 | 1614 | U31281 | Corynebacterium glutamicum biotin synthase (bioB) gene, complete cds. | Corynebacterium glutamicum | 99,111 | 21-Nov-96 |
| GB_BA1:BRLBIOBA | 1647 | D14084 | Brevibacterium flavum gene for biotin synthetase, complete cds. | Corynebacterium glutamicum | 98,489 | 3-Feb-99 |
| GB_PAT:E03937 | 1005 | E03937 | DNA sequence encoding Brevibacterium flavum biotin-synthase. | Corynebacterium glutamicum | 98,207 | 29-Sep-97 |
| GB_BA1:MTCY427 | 38110 | Z70692 | Mycobacterium tuberculosis H37Rv complete genome; segment 99/162. | Mycobacterium tuberculosis | 35,615 | 24-Jun-99 |
| GB_BA1:MSGB32CS | 36404 | L78818 | Mycobacterium leprae cosmid B32 DNA sequence. | Mycobacterium leprae | 60,917 | 15-Jun-96 |
| GB_BA1:MTCY427 | 38110 | Z70692 | Mycobacterium tuberculosis H37Rv complete genome; segment 99/162. | Mycobacterium tuberculosis | 44,606 | 24-Jun-99 |
| GB_BA1:MSGB32CS | 36404 | L78818 | Mycobacterium leprae cosmid B32 DNA sequence. | Mycobacterium leprae | 52,516 | 15-Jun-96 |
| GB_BA1:MTCY427 | 38110 | Z70692 | Mycobacterium tuberculosis H37Rv complete genome; segment 99/162. | Mycobacterium tuberculosis | 38,079 | 24-Jun-99 |
| GB_OM:BOVELA | 3242 | J02717 | Bovine elastin a mRNA, complete cds. | Bos taurus | 39,351 | 27-Apr-93 |
| GB_BA1:CGTHRC | 3120 | X56037 | Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2). | Corynebacterium glutamicum | 99,808 | 17-Jun-97 |
| GB_PAT:I09078 | 3146 | I09078 | Sequence 4 from Patent WO 8809819. | Unknown. | 99,617 | 02-DEC-1994 |
| GB_BA1:BLTHRESYN | 1892 | Z29563 | Brevibacterium lactofermentum; ATCC 13869; DNA (genomic);. | Corynebacterium glutamicum | 99,170 | 20-Sep-95 |
| GB_BA1:CGGLNA | 3686 | Y13221 | Corynebacterium glutamicum glnA gene. | Corynebacterium glutamicum | 100,000 | 28-Aug-97 |
| GB_BA2:AF005635 | 1690 | AF005635 | Corynebacterium glutamicum glutamine synthetase (glnA) gene, complete cds. | Corynebacterium glutamicum | 98,906 | 14-Jun-99 |
| GB_BA1:MSGB27CS | 38793 | L78817 | Mycobacterium leprae cosmid B27 DNA sequence. | Mycobacterium leprae | 66,345 | 15-Jun-96 |
| GB_EST27:AI455217 | 624 | AI455217 | LD21828.3prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD21828 3prime, mRNA sequence. | Drosophila melanogaster | 34,510 | 09-MAR-1999 |
| GB_BA2:SSU30252 | 2891 | U30252 | Synechococcus PCC7942 nucleoside diphosphate kinase and ORF2 protein genes, complete cds, ORF1 protein gene, partial cds, and neutral site 1 for vector use. | Synechococcus PCC7942 | 37,084 | 29-OCT-1999 |
| GB_EST21:AA911262 | 581 | AA911262 | oe75a02 s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1417418 3' similar to gb:A18757 UROKINASE PLASMINOGEN ACTIVATOR SURFACE RECEPTOR, GPI-ANCHORED (HUMAN);, mRNA sequence. | Homo sapiens | 37,500 | 21-Apr-98 |
| GB_BA1:MLU15187 | 36138 | U15187 | Mycobacterium leprae cosmid L296. | Mycobacterium leprae | 52,972 | 09-MAR-1995 |
| GB_IN2:AC004373 | 72722 | AC004373 | Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence. | Drosophila melanogaster | 46,341 | 17-Jul-98 |
| GB_IN2:AF145653 | 3197 | AF145653 | Drosophila melanogaster clone GH08860 BcDNA.GH08860 (BcDNA.GH08860) mRNA, complete cds. | Drosophila melanogaster | 49,471 | 14-Jun-99 |
| GB_BA1:AB024708 | 8734 | AB024708 | Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds | Corynebacterium glutamicum | 96,556 | 13-MAR-1999 |
| GB_BA1:MTCY1A6 | 37751 | Z83864 | Mycobacterium tuberculosis H37Rv complete genome; segment 159/162. | Mycobacterium tuberculosis | 39,496 | 17-Jun-98 |
| GB_BA1:SC3A3 | 15901 | AL109849 | Streptomyces coelicolor cosmid 3A3. | Streptomyces coelicolor A3(2) | 37,946 | 16-Aug-99 |
| GB_BA1:AB024708 | 8734 | AB024708 | Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds. | Corynebacterium glutamicum | 99,374 | 13-MAR-1999 |
| GB_BA1:MTCY1A6 | 37751 | Z83864 | Mycobacterium tuberculosis H37Rv complete genome; segment 159/162. | Mycobacterium tuberculosis | 41,333 | 17-Jun-98 |
| GB_BA1:SC3A3 | 15901 | AL109849 | Streptomyces coelicolor cosmid 3A3. | Streptomyces coelicolor A3(2) | 37,554 | 16-Aug-99 |

TABLE 4: ALIGNMENT RESULTS

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|---------|------|-------------------|--------|----------|---|---|--------|-------------|
| rx00367 | 4653 | GB_BA1:AB024708 | 8734 | AB024708 | Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds. | Corynebacterium glutamicum | 99,312 | 13-MAR-1999 |
| | | GB_BA1:MTCY1A6 | 37751 | Z83864 | Mycobacterium tuberculosis H37Rv complete genome; segment 159/162. | Mycobacterium tuberculosis | 36,971 | 17-Jun-98 |
| | | GB_BA1:SC3A3 | 15901 | AL109849 | Streptomyces coelicolor cosmid 3A3. | Streptomyces coelicolor A3(2) | 37,905 | 16-Aug-99 |
| rx00371 | 1917 | GB_VI:SBVORFS | 7568 | M89923 | Sugarcane bacilliform virus ORF 1,2, and 3 DNA, complete cds. | Sugarcane bacilliform virus | 35,843 | 12-Jun-93 |
| | | GB_EST37:AI967505 | 380 | AI967505 | Ljirpest03-215-c10 Ljirmp Lambda HybriZap two-hybrid library Lotus japonicus cDNA clone LP215-03-c10 5' similar to 60S ribosomal protein L39, mRNA sequence. | Lotus japonicus | 42,593 | 24-Aug-99 |
| rx00377 | 1245 | GB_IN1:CELK09H9 | 37881 | AF043700 | Caenorhabditis elegans cosmid K09H9. | Caenorhabditis elegans | 34,295 | 22-Jan-98 |
| | | GB_BA1:CCU13664 | 1678 | U13664 | Caulobacter crescentus uroporphyrinogen decarboxylase homolog (hemE) gene, partial cds. | Caulobacter crescentus | 36,832 | 24-MAR-1995 |
| | | GB_PL1:ANSDGENE | 1299 | Y08866 | A. nidulans sD gene. | | | |
| | | GB_GSS4:AQ730303 | 483 | AQ730303 | HS_5505_B1_C04_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1081 Col=7 Row=F, genomic survey sequence. | Homo sapiens | 39,603 | 17-OCT-1996 |
| rx00382 | 1425 | GB_BA1:PAHEML | 4444 | X82072 | P. aeruginosa hemL gene. | | 36,728 | 15-Jul-99 |
| | | GB_BA1:MTY25D10 | 40838 | Z95558 | Mycobacterium tuberculosis H37Rv complete genome; segment 28/162. | Pseudomonas aeruginosa | 54,175 | 18-DEC-1995 |
| | | GB_BA1:MSGY224 | 40051 | AD000004 | Mycobacterium tuberculosis sequence from clone y224. | Mycobacterium tuberculosis | 61,143 | 17-Jun-98 |
| rx00383 | 1467 | GB_BA1:MLCB1222 | 34714 | AL049491 | Mycobacterium leprae cosmid B1222. | Mycobacterium tuberculosis | 61,143 | 03-DEC-1996 |
| | | GB_HTG2:AC006269 | 167171 | AC006269 | Homo sapiens chromosome 17 clone hRPK.515_E_23 map 17, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces. | Mycobacterium leprae | 43,981 | 27-Aug-99 |
| | | | | | Homo sapiens chromosome 17 clone hRPK.515_O_17 map 17, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces. | Homo sapiens | 35,444 | 10-Jun-99 |
| rx00391 | 843 | GB_EST38:AW017053 | 613 | AW017053 | EST727398 Schistosoma mansoni male, Phil LoVerde/Joel Merrick | Homo sapiens | 34,821 | 22-MAY-1999 |
| | | GB_PAT:AR065852 | 32207 | AR065852 | Schistosoma mansoni cDNA clone SMMAS14 5' end, mRNA sequence. | Schistosoma mansoni | 40,472 | 10-Sep-99 |
| | | GB_VI:AF148805 | 28559 | AF148805 | Sequence 20 from patent US 5849564. | Unknown. | 38,586 | 29-Sep-99 |
| | | | | | Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds. | Kaposi's sarcoma-associated herpesvirus | 38,509 | 2-Aug-99 |
| rx00393 | 1017 | GB_BA1:MTY25D10 | 40838 | Z95558 | Mycobacterium tuberculosis H37Rv complete genome; segment 28/162. | Mycobacterium tuberculosis | 36,308 | 17-Jun-98 |
| | | GB_BA1:MSGY224 | 40051 | AD000004 | Mycobacterium tuberculosis sequence from clone y224. | Mycobacterium tuberculosis | 39,282 | 03-DEC-1996 |
| | | GB_BA1:MLB1306 | 7762 | Y13803 | Mycobacterium leprae cosmid B1306 DNA. | Mycobacterium leprae | 39,228 | 24-Jun-97 |
| rx00402 | 623 | GB_BA2:AF052652 | 2096 | AF052652 | Corynebacterium glutamicum homoserine O-acetyltransferase (metA) gene, complete cds. | Corynebacterium glutamicum | 99,672 | 19-MAR-1998 |
| | | GB_BA2:AF109162 | 4514 | AF109162 | Corynebacterium diphtheriae heme uptake locus, complete sequence. | Corynebacterium glutamicum | 99,920 | 19-MAR-1998 |
| | | GB_BA2:AF092918 | 20758 | AF092918 | Pseudomonas alcaligenes outer membrane Xcp-secretion system gene cluster. | Corynebacterium diphtheriae | 40,830 | 8-Jun-99 |
| rx00403 | 1254 | GB_BA2:AF052652 | 2096 | AF052652 | Corynebacterium glutamicum homoserine O-acetyltransferase (metA) gene, complete cds. | Pseudomonas alcaligenes | 50,161 | 06-DEC-1998 |
| | | GB_BA1:MTV016 | 53662 | AL021841 | Mycobacterium tuberculosis H37Rv complete genome; segment 143/162. | Corynebacterium glutamicum | 99,920 | 19-MAR-1998 |
| | | GB_EST23:AI111288 | 750 | AI111288 | SWOVAMCAQ02A05SK Onchocerca volvulus adult male cDNA (SAW98MLW-OvAM) Onchocerca volvulus cDNA clone SWOVAMCAQ02A05 5', mRNA sequence. | Mycobacterium tuberculosis | 52,898 | 23-Jun-99 |
| | | | | | | Onchocerca volvulus | 37,565 | 31-Aug-98 |

TABLE 4: ALIGNMENT RESULTS

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|---------|------|---|--|--|---|--|--|---|
| rx00405 | 613 | GB_BA1:MTV016 GB_PR4:AC005145 | 53662 143678 | AL021841 AC005145 | Mycobacterium tuberculosis H37Rv complete genome; segment 143/162. Homo sapiens Xp22-166-169 GSHB-523A23 (Genome Systems Human BAC library) complete sequence. | Mycobacterium tuberculosis Homo sapiens | 57,259 34,179 | 23-Jun-99 08-DEC-1998 |
| rx00420 | 1587 | GB_BA1:MTV016 GB_BA1:MTY13D12 GB_BA1:MSGY126 GB_BA1:MSGB971CS GB_BA1:AFACBBTZ | 53662 37085 37164 37566 2760 | AL021841 Z80343 AD000012 L78821 M68904 | Mycobacterium tuberculosis H37Rv complete genome; segment 143/162. Mycobacterium tuberculosis H37Rv complete genome; segment 156/162. Mycobacterium tuberculosis sequence from clone y126. Mycobacterium leprae cosmid B971 DNA sequence. Alcaligenes eutrophus chromosomal transketolase (cbbTc) and phosphoglycolate phosphatase (cbbZc) genes, complete cds. | Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium leprae Ralstonia eutropha | 40,169 62,031 61,902 39,651 38,677 | 23-Jun-99 17-Jun-98 10-DEC-1996 15-Jun-96 27-Jul-94 |
| rx00435 | 1296 | GB_HTG4:AC009541 | 169583 | AC009541 | Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces. | Homo sapiens | 36,335 | 12-OCT-1999 |
| rx00437 | 579 | GB_HTG4:AC009541 GB_PR4:AC005951 | 169583 155450 | AC009541 AC005951 | Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces. Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence. | Homo sapiens Homo sapiens | 36,335 31,738 | 12-OCT-1999 18-Nov-98 |
| rx00439 | 591 | GB_BA1:MTV016 GB_PL2:AF167358 GB_HTG3:AC009120 | 53662 1022 269445 | AL021841 AF167358 AC009120 | Mycobacterium tuberculosis H37Rv complete genome; segment 143/162. Rumex acetosa expansin (EXP3) gene, partial cds. Homo sapiens chromosome 16 clone RPCI-11_484E3, *** SEQUENCING IN PROGRESS ***, 34 unordered pieces. | Mycobacterium tuberculosis Rumex acetosa Homo sapiens | 37,088 46,538 43,276 | 23-Jun-99 17-Aug-99 3-Aug-99 |
| rx00440 | 582 | GB_BA2:SKZ86111 | 7860 | Z86111 | Streptomyces lividans rpsP, trmD, rplS, sipW, sipX, sipY, sipZ, mutT genes and 4 open reading frames. | Streptomyces lividans | 43,080 | 27-OCT-1999 |
| rx00441 | 1287 | GB_BA1:SC2E1 GB_BA1:SC2E1 GB_PR2:HS173D1 | 38962 38962 117338 | AL023797 AL023797 AL031984 | Streptomyces coelicolor cosmid 2E1. Streptomyces coelicolor cosmid 2E1. Human DNA sequence from clone 173D1 on chromosome 1p36.21-36.33. Contains ESTs, STS and GSSs, complete sequence. | Streptomyces coelicolor Streptomyces coelicolor Homo sapiens | 42,931 36,702 38,027 | 4-Jun-98 4-Jun-98 23-Nov-99 |
| rx00446 | 987 | GB_HTG2:HSDJ719K3 GB_HTG2:HSDJ719K3 GB_HTG2:AF029367 GB_HTG4:AC009367 | 267114 267114 226055 226055 | AL109931 AL109931 AL034355 AC009367 | Homo sapiens chromosome X clone RP4-719K3 map q21.1-21.31, *** SEQUENCING IN PROGRESS ***, in unordered pieces. Homo sapiens chromosome X clone RP4-719K3 map q21.1-21.31, *** SEQUENCING IN PROGRESS ***, in unordered pieces. Streptomyces coelicolor cosmid D78. | Homo sapiens Homo sapiens Streptomyces coelicolor | 34,521 34,521 56,410 | 03-DEC-1999 03-DEC-1999 26-Nov-98 |
| rx00448 | 1143 | GB_HTG4:AC009367 GB_HTG4:AC009367 GB_HTG4:AC009367 GB_HTG4:AC009367 | 226055 226055 226055 226055 | AC009367 AC009367 AC009367 AC009367 | Drosophila melanogaster chromosome 3L/76A2 clone RPCI98-48B15, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces. Drosophila melanogaster chromosome 3L/76A2 clone RPCI98-48B15, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces. Homo sapiens 12q13.1 PAC RPCI1-130F5 (Roswell Park Cancer Institute Human PAC library) complete sequence. | Drosophila melanogaster Drosophila melanogaster Homo sapiens | 34,959 34,959 35,682 | 16-OCT-1999 16-OCT-1999 9-Jun-98 |
| rx00449 | 1143 | GB_HTG2:AF029367 GB_HTG2:AF029367 GB_HTG2:AF029367 | 148676 148676 148676 | AF029367 AF029367 AF029367 | Homo sapiens chromosome 12 clone RPCI-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS ***, 156 unordered pieces. Homo sapiens chromosome 12 clone RPCI-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS ***, 156 unordered pieces. | Homo sapiens Homo sapiens Homo sapiens | 31,373 31,373 31,373 | 18-OCT-1997 18-OCT-1997 18-OCT-1997 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|-------------------|--------|----------|--|-----------------------------|---------|-------------|
| rx00450 | 424 | GB_HTG2:AC007824 | 133361 | AC007824 | Drosophila melanogaster chromosome 3 clone BACR02L16 (D715) RPCI-98 02.L.16 map 89E-90A strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 91 unordered pieces. | Drosophila melanogaster | 40,000 | 2-Aug-99 |
| | | GB_HTG2:AC007824 | 133361 | AC007824 | Drosophila melanogaster chromosome 3 clone BACR02L16 (D715) RPCI-98 02.L.16 map 89E-90A strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 91 unordered pieces. | Drosophila melanogaster | 40,000 | 2-Aug-99 |
| | | GB_EST35:A1818057 | 412 | A1818057 | wk14a08.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2412278 3' similar to gb:Y00764 UBQUINOL-CYTOCHROME C REDUCTASE 11 KD PROTEIN (HUMAN); mRNA sequence. | Homo sapiens | 35,714 | 24-Aug-99 |
| rx00461 | 975 | GB_BA1:MLCB1779 | 43254 | Z98271 | Mycobacterium leprae cosmid B1779. | Mycobacterium leprae | 39,308 | 8-Aug-97 |
| | | GB_IN1:DMC85E4 | 29352 | AL021086 | Drosophila melanogaster cosmid clone 86E4. | Drosophila melanogaster | 37,487 | 27-Apr-99 |
| rx00465 | | GB_GSS15:AQ640325 | 467 | AQ640325 | 927P1-2H3.TP 927P1 Trypanosoma brucei genomic clone 927P1-2H3, genomic survey sequence. | Trypanosoma brucei | 38,116 | 8-Jul-99 |
| rx00487 | 1692 | GB_BA1:BAGUAA | 3866 | Y10499 | B.ammoniaenes guaA gene. | Corynebacterium ammoniaenes | 74,259 | 8-Jan-98 |
| | | GB_BA2:U00015 | 42325 | U00015 | Mycobacterium leprae cosmid B1620. | Mycobacterium leprae | 37,248 | 01-MAR-1994 |
| rx00488 | 1641 | GB_BA1:MTCY78 | 33818 | Z77165 | Mycobacterium tuberculosis H37Rv complete genome, segment 145/162. | Mycobacterium tuberculosis | 39,725 | 17-Jun-98 |
| | | GB_BA1:MTCY78 | 33818 | Z77165 | Mycobacterium tuberculosis H37Rv complete genome; segment 145/162. | Mycobacterium tuberculosis | 39,451 | 17-Jun-98 |
| | | GB_BA2:U00015 | 42325 | U00015 | Mycobacterium leprae cosmid B1620. | Mycobacterium leprae | 39,178 | 01-MAR-1994 |
| | | GB_BA1:SCAJ10601 | 4692 | AJ010601 | Streptomyces coelicolor A3(2) DNA for whiI and whiK loci. | Streptomyces coelicolor | 60,835 | 17-Sep-98 |
| rx00489 | 1245 | GB_BA2:U00015 | 42325 | U00015 | Mycobacterium leprae cosmid B1620. | Mycobacterium leprae | 38,041 | 01-MAR-1994 |
| | | GB_HTG2:HS225E12 | 126464 | AL031772 | Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS ***; in unordered pieces. | Homo sapiens | 36,756 | 03-DEC-1999 |
| | | GB_HTG2:HS225E12 | 126464 | AL031772 | Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS ***; in unordered pieces. | Homo sapiens | 36,756 | 03-DEC-1999 |
| rx00533 | 1155 | GB_BA1:CGLYS | 2803 | X57226 | C. glutamicum lysC-alpha, lysC-beta and asd genes for aspartokinase-alpha and -beta subunits, and aspartate beta semialdehyde dehydrogenase, respectively (EC 2.7.2.4; EC 1.2.1.11) | Corynebacterium glutamicum | 99,913 | 17-Feb-97 |
| | | GB_BA1:CGCYSCASD | 1591 | X82928 | C.glutamicum aspartate-semialdehyde dehydrogenase gene. | Corynebacterium glutamicum | 99,221 | 17-Feb-97 |
| rx00534 | 1386 | GB_PAT:A07546 | 2112 | A07546 | Recombinant DNA fragment (PstI-XhoI). | synthetic construct | 99,391 | 30-Jul-93 |
| | | GB_BA1:CGLYS | 2803 | X57226 | C. glutamicum lysC-alpha, lysC-beta and asd genes for aspartokinase-alpha and -beta subunits, and aspartate beta semialdehyde dehydrogenase, respectively (EC 2.7.2.4; EC 1.2.1.11). | Corynebacterium glutamicum | 99,856 | 17-Feb-97 |
| | | GB_BA1:CORASKD | 2957 | L16848 | Corynebacterium flavum aspartokinase (ask), and aspartate-semialdehyde dehydrogenase (asd) genes, complete cds. | Corynebacterium flavesceus | 98,701 | 11-Jun-93 |
| rx00536 | 1494 | GB_PAT:E14514 | 1643 | E14514 | DNA encoding Brevibacterium aspartokinase. | Corynebacterium glutamicum | 98,773 | 28-Jul-99 |
| | | GB_BA1:CGLEUA | 3492 | X70959 | C.glutamicum gene leuA for isopropylmalate synthase. | Corynebacterium glutamicum | 100,000 | 10-Feb-99 |
| | | GB_BA1:MTV025 | 121125 | AL022121 | Mycobacterium tuberculosis H37Rv complete genome; segment 155/162. | Mycobacterium tuberculosis | 68,003 | 24-Jun-99 |
| | | GB_BA1:MTU88526 | 2412 | U88526 | Mycobacterium tuberculosis putative alpha-isopropyl malate synthase (leuA) gene, complete cds. | Mycobacterium tuberculosis | 68,185 | 26-Feb-97 |

TABLE 4: ALIGNMENT RESULTS

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|---------|------|-------------------|-------|----------|---|-----------------------------------|--------|--------------------|
| rx00537 | 2409 | GB_BA2:SCD25 | 41622 | AL118514 | Streptomyces coelicolor cosmid D25. | Streptomyces coelicolor A3(2) | 63,187 | 21-Sep-99 |
| rx00541 | 792 | GB_BA1:MTCY7H7A | 10451 | Z95618 | Mycobacterium tuberculosis H37Rv complete genome; segment 39/162. | Mycobacterium tuberculosis | 62,401 | 17-Jun-98 |
| | | GB_BA1:MTU34956 | 2462 | U34956 | Mycobacterium tuberculosis phosphoribosylformylglycinamide synthase (purL) gene, complete cds. | Mycobacterium tuberculosis | 62,205 | 28-Jan-97 |
| | | GB_PAT:I92052 | 2115 | I92052 | Sequence 19 from patent US 5726299. | Unknown. | 98,359 | 01-DEC-1998 |
| rx00558 | 1470 | GB_BA1:MLCB5 | 38109 | Z95151 | Mycobacterium leprae cosmid B5. | Mycobacterium leprae | 62,468 | 24-Jun-97 |
| | | GB_BA1:MTCY369 | 36850 | Z80226 | Mycobacterium tuberculosis H37Rv complete genome; segment 36/162. | Mycobacterium tuberculosis | 60,814 | 17-Jun-98 |
| | | GB_BA1:BAPURF | 1885 | X91252 | B.ammoniaenes purF gene | Corynebacterium ammoniagenes | 66,095 | 5-Jun-97 |
| | | GB_BA1:MLU15182 | 40123 | U15182 | Mycobacterium leprae cosmid B2266. | Mycobacterium leprae | 64,315 | 09-MAR-1995 |
| rx00579 | 1983 | GB_BA1:MTCY7H7A | 10451 | Z95618 | Mycobacterium tuberculosis H37Rv complete genome; segment 39/162. | Mycobacterium tuberculosis | 64,863 | 17-Jun-98 |
| | | GB_PAT:AR016483 | 2104 | AR016483 | Sequence 1 from patent US 5776740 | Unknown. | 98,810 | 05-DEC-1998 |
| | | EM_PAT:E11273 | 2104 | E11273 | DNA encoding serine hydroxymethyl transferase. | Corynebacterium glutamicum | 98,810 | 08-OCT-1997 |
| | | GB_PAT:E12594 | 2104 | E12594 | DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum. | Corynebacterium glutamicum | 98,810 | (Rel. 52, Created) |
| rx00580 | 1425 | GB_PAT:E12594 | 2104 | E12594 | DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum. | Corynebacterium glutamicum | 98,810 | 24-Jun-98 |
| | | GB_PAT:AR016483 | 2104 | AR016483 | Sequence 1 from patent US 5776740. | Corynebacterium glutamicum | 99,368 | 24-Jun-98 |
| | | EM_PAT:E11273 | 2104 | E11273 | DNA encoding serine hydroxymethyl transferase. | Unknown. | 99,368 | 05-DEC-1998 |
| | | GB_PAT:E12594 | 2104 | E12594 | DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum. | Corynebacterium glutamicum | 99,368 | 08-OCT-1997 |
| rx00581 | 1092 | EM_PAT:E11273 | 2104 | E11273 | DNA encoding serine hydroxymethyl transferase. | Corynebacterium glutamicum | 37,071 | (Rel. 52, Created) |
| | | GB_PAT:E12594 | 2104 | E12594 | DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum. | Corynebacterium glutamicum | 37,071 | 24-Jun-98 |
| rx00584 | 1248 | GB_PAT:AR016483 | 2104 | AR016483 | Sequence 1 from patent US 5776740. | Unknown. | 37,071 | 08-OCT-1997 |
| | | GB_BA1:CORAHPS | 2570 | L07603 | Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene, complete cds. | Corynebacterium glutamicum | 98,236 | (Rel. 52, Created) |
| rx00618 | 1230 | GB_BA1:AOPCZA361 | 37941 | AJ223998 | Amycolatopsis orientalis cosmid PCZA361. | Amycolatopsis orientalis | 54,553 | 29-MAR-1999 |
| | | GB_BA1:D90714 | 14358 | D90714 | Escherichia coli genomic DNA. (16.8 - 17.1 min). | Escherichia coli | 53,312 | 7-Feb-99 |
| | | GB_EST19:AA802737 | 280 | AA802737 | GM06236.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM06236 5prime, mRNA sequence. | Drosophila melanogaster | 39,928 | 25-Nov-98 |
| | | GB_EST28:AI534381 | 581 | AI534381 | SD07186.5prime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster cDNA clone SD07186 5prime similar to X89858; Ani FBgn0011558 PID:g927407 SPTREMBL.Q24240, mRNA sequence. | Drosophila melanogaster | 41,136 | 18-MAR-1999 |
| | | GB_IN1:DMANILLIN | 4029 | X89858 | D.melanogaster mRNA for anillin protein. | Drosophila melanogaster | 34,398 | 8-Nov-95 |
| rx00619 | 1551 | GB_BA1:MTCY369 | 36850 | Z80226 | Mycobacterium tuberculosis H37Rv complete genome; segment 36/162. | Mycobacterium tuberculosis | 62,776 | 17-Jun-98 |
| | | GB_BA1:MLCB5 | 38109 | Z95151 | Mycobacterium leprae cosmid B5. | Mycobacterium leprae | 61,831 | 24-Jun-97 |
| | | GB_PAT:A60305 | 1845 | A60305 | Sequence 5 from Patent WO9708323. | unidentified | 61,785 | 06-MAR-1998 |
| | | GB_PL2:AF063247 | 1450 | AF063247 | Pneumocystis carinii f. sp. ratti enolase mRNA, complete cds. | Pneumocystis carinii f. sp. ratti | 41,060 | 5-Jan-99 |
| rx00620 | 1014 | GB_BA1:STMAPP | 2069 | M91546 | Streptomyces lividans aminopeptidase P (PepP) gene, complete cds. | Streptomyces lividans | 37,126 | 12-Jun-93 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|-------------------|--------|----------|--|----------------------------|--------|-------------|
| rx00624 | 810 | GB_HTG3:AC008763 | 214575 | AC008763 | Homo sapiens chromosome 19 clone CITB-E1_3214H19, *** SEQUENCING IN PROGRESS ***; 21 unordered pieces. | Homo sapiens | 40,020 | 3-Aug-99 |
| | | GB_IN1:CEY41E3 | 150641 | Z95559 | Caenorhabditis elegans cosmid Y41E3, complete sequence. | Caenorhabditis elegans | 36,986 | 2-Sep-99 |
| | | GB_EST13:AA362167 | 372 | AA362167 | EST71561 Macrophage I Homo sapiens cDNA 5' end, mRNA sequence. | Homo sapiens | 38,378 | 21-Apr-97 |
| | | GB_IN1:CEY41E3 | 150641 | Z95559 | Caenorhabditis elegans cosmid Y41E3, complete sequence. | Caenorhabditis elegans | 37,694 | 2-Sep-99 |
| rx00626 | 1386 | GB_BA1:MTCY369 | 36850 | Z80226 | Mycobacterium tuberculosis H37Rv complete genome; segment 36/162. | Mycobacterium tuberculosis | 57,971 | 17-Jun-98 |
| | | GB_BA1:MLCB5 | 38109 | Z95151 | Mycobacterium leprae cosmid B5. | Mycobacterium leprae | 58,806 | 24-Jun-97 |
| | | GB_BA1:MLU15187 | 36138 | U15187 | Mycobacterium leprae cosmid L296. | Mycobacterium leprae | 38,007 | 09-MAR-1995 |
| rx00632 | 795 | GB_BA1:BRLBIOAD | 2272 | D14083 | Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds. | Corynebacterium glutamicum | 97,358 | 3-Feb-99 |
| | | GB_PAT:E04041 | 675 | E04041 | DNA sequence coding for dethiobiotin synthetase. | Corynebacterium glutamicum | 98,074 | 29-Sep-97 |
| | | GB_PAT:E04040 | 1272 | E04040 | DNA sequence coding for diamino pelargonic acid aminotransferase. | Corynebacterium glutamicum | 93,814 | 29-Sep-97 |
| rx00633 | 1392 | GB_BA1:BRLBIOAD | 2272 | D14083 | Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds. | Corynebacterium glutamicum | 95,690 | 3-Feb-99 |
| | | GB_PAT:E04040 | 1272 | E04040 | DNA sequence coding for diamino pelargonic acid aminotransferase. | Corynebacterium glutamicum | 95,755 | 29-Sep-97 |
| | | GB_BA2:EHU38519 | 1290 | U38519 | Erwinia herbicola adenosylmethionine-8-amino-7-oxononanoate transaminase (bioA) gene, complete cds. | Erwinia herbicola | 55,564 | 4-Nov-96 |
| rx00688 | 666 | GB_BA1:MTV041 | 28826 | AL021958 | Mycobacterium tuberculosis H37Rv complete genome; segment 35/162. | Mycobacterium tuberculosis | 60,030 | 17-Jun-98 |
| | | GB_BA1:BRLSECY | 1516 | D14162 | Brevibacterium flavum gene for SecY protein (complete cds) and gene or adenylate kinase (partial cds). | Corynebacterium glutamicum | 99,563 | 3-Feb-99 |
| | | GB_BA2:MBU77912 | 7163 | U77912 | Mycobacterium bovis MBE50a gene, partial cds; and MBE50b, MBE50c, preprotein translocase SecY subunit (secY), adenylate kinase (adk), methionine aminopeptidase (map), RNA polymerase ECF sigma factor (sigE50), MBE50d, and MBE50e genes, complete cds. | Mycobacterium bovis | 60,030 | 27-Jan-99 |
| rx00708 | 930 | GB_BA2:AF157493 | 25454 | AF157493 | Zymomonas mobilis ZM4 fosmid clone 42D7, complete sequence. | Zymomonas mobilis | 39,116 | 5-Jul-99 |
| | | GB_PAT:I00836 | 1853 | I00836 | Sequence 1 from Patent US 4758514. | Unknown. | 47,419 | 21-MAY-1993 |
| | | GB_PAT:E00311 | 1853 | E00311 | DNA coding of 2,5-diketogluconic acid reductase. | unidentified | 47,419 | 29-Sep-97 |
| rx00717 | 1083 | GB_PAT:I78753 | 1187 | I78753 | Sequence 9 from patent US 5693781. | Unknown. | 37,814 | 3-Apr-98 |
| | | GB_PAT:I92042 | 1187 | I92042 | Sequence 9 from patent US 5726299. | Unknown. | 37,814 | 01-DEC-1998 |
| | | GB_BA1:MTG125 | 37432 | Z98268 | Mycobacterium tuberculosis H37Rv complete genome; segment 76/162. | Mycobacterium tuberculosis | 50,647 | 17-Jun-98 |
| rx00718 | 831 | GB_BA1:MTG125 | 37432 | Z98268 | Mycobacterium tuberculosis H37Rv complete genome; segment 76/162. | Mycobacterium tuberculosis | 55,228 | 17-Jun-98 |
| | | GB_BA1:MTG125 | 37432 | Z98268 | Mycobacterium tuberculosis H37Rv complete genome; segment 76/162. | Mycobacterium tuberculosis | 40,300 | 17-Jun-98 |
| | | GB_GSS12:AQ420755 | 671 | AQ420755 | RPCI-11-168G18.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-168G18, genomic survey sequence. | Homo sapiens | 35,750 | 23-MAR-1999 |
| rx00727 | 1035 | GB_HTG3:AC008332 | 118545 | AC008332 | Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCI-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 78 unordered pieces. | Drosophila melanogaster | 40,634 | 6-Aug-99 |
| | | GB_HTG3:AC008332 | 118545 | AC008332 | Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCI-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***; 78 unordered pieces. | Drosophila melanogaster | 40,634 | 6-Aug-99 |
| | | GB_HTG3:AC008332 | 118545 | AC008332 | Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCI-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***; 78 unordered pieces. | Drosophila melanogaster | 33,888 | 6-Aug-99 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | |
|---------|------|-------------------|--------|----------|---|---------|-------------|
| rx00766 | 966 | GB_HTG2:AC006789 | 83823 | AC006789 | Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS ***; 2 Caenorhabditis elegans unordered pieces. | 36,737 | 25-Feb-99 |
| | | GB_HTG2:AC006789 | 83823 | AC006789 | Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS ***; 2 Caenorhabditis elegans unordered pieces. | 36,737 | 25-Feb-99 |
| rx00770 | 1293 | GB_BA1:D90810 | 20476 | D90810 | E.coli genomic DNA, Kohara clone #319(37.4-37.8 min.). | 36,526 | 29-MAY-1997 |
| | | GB_BA1:MTV043 | 68848 | AL022004 | Mycobacterium tuberculosis H37Rv complete genome; segment 40/162. | 66,193 | 24-Jun-99 |
| | | GB_BA1:MLU15182 | 40123 | U15182 | Mycobacterium leprae cosmid B2286. | 61,443 | 09-MAR-1995 |
| | | GB_BA2:SCD25 | 41622 | AL118514 | Streptomyces coelicolor cosmid D25. | 59,938 | 21-Sep-99 |
| rx00779 | 1056 | GB_HTG1:CER08A5 | 51920 | Z82281 | Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***; in unordered pieces. | 64,896 | 14-OCT-1998 |
| | | GB_HTG1:CER08A5 | 51920 | Z82281 | Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***; in unordered pieces. | 64,896 | 14-OCT-1998 |
| | | GB_PL2:AF078693 | 1492 | AF078693 | Chlamydomonas reinhardtii putative O-acetylserine(thiol)lyase precursor (Crcys-1A) mRNA, nuclear gene encoding organellar protein, complete cds. | 57,970 | 3-Nov-99 |
| rx00780 | 669 | GB_BA1:MTCY98 | 31225 | Z83860 | Mycobacterium tuberculosis H37Rv complete genome; segment 103/162. | 54,410 | 17-Jun-98 |
| | | GB_BA1:AVINIFREG | 7099 | M60090 | Azotobacter chroococcum nifU, nifS, nifV, nifP, nifW, nifZ and nifM genes, complete cds. | 51,729 | 26-Apr-93 |
| rx00838 | 1023 | GB_BA2:AF001780 | 6701 | AF001780 | Cyanotheca PCC 8801 NifP (nifP), nitrogenase (nifB), FdxN (fdxN), NifS (nifS) and NifU (nifU) genes, complete cds, and NifH (nifH) gene, partial cds. | 36,309 | 08-MAR-1999 |
| | | GB_EST1:Z30506 | 329 | Z30506 | ATTS2430 AC16H Arabidopsis thaliana cDNA clone TAI306 3', mRNA sequence. | 44,308 | 11-MAR-1994 |
| | | GB_PL2:AC006258 | 110469 | AC006258 | Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence. | 35,571 | 28-DEC-1998 |
| | | GB_EST37:AI998439 | 455 | AI998439 | 701545695 A. thaliana, Columbia Col-0, rosette-2 Arabidopsis thaliana cDNA clone 701545695, mRNA sequence. | 36,044 | 8-Sep-99 |
| rx00863 | 867 | GB_BA1:BLDAPAB | 3572 | Z21502 | B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase. | 99,539 | 16-Aug-93 |
| | | GB_PAT:E16749 | 2001 | E16749 | gDNA encoding dihydrodipicolinate synthase (DDPS). | 99,539 | 28-Jul-99 |
| | | GB_PAT:E14520 | 2001 | E14520 | DNA encoding Brevibacterium dihydrodipicolinic acid synthase. | 99,539 | 28-Jul-99 |
| rx00864 | 873 | GB_BA1:BLDAPAB | 3572 | Z21502 | B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase. | 99,885 | 16-Aug-93 |
| | | GB_BA1:CGDAPB | 1902 | X67737 | C.glutamicum dapB gene for dihydrodipicolinate reductase. | 100,000 | 1-Apr-93 |
| | | GB_PAT:E14520 | 2001 | E14520 | DNA encoding Brevibacterium dihydrodipicolinic acid synthase. | 100,000 | 28-Jul-99 |
| rx00865 | 1026 | GB_BA1:BLDAPAB | 3572 | Z21502 | B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase. | 100,000 | 16-Aug-93 |
| | | GB_PAT:E16752 | 1411 | E16752 | gDNA encoding dihydrodipicolinate reductase (DDPR). | 99,805 | 28-Jul-99 |
| | | GB_PAT:AF038113 | 1411 | AR038113 | Sequence 18 from patent US 5804414. | 99,805 | 29-Sep-99 |
| rx00867 | 650 | GB_BA1:MTV002 | 56414 | AL008967 | Mycobacterium tuberculosis H37Rv complete genome; segment 122/162. | 39,179 | 17-Jun-98 |
| | | GB_BA1:MLCB22 | 40281 | Z98741 | Mycobacterium leprae cosmid B22. | 39,482 | 22-Aug-97 |
| | | GB_BA1:SAU19858 | 2838 | U19858 | Streptomyces antibioticus guanosine pentaphosphate synthetase (gpsI) gene, complete cds. | 69,706 | 25-OCT-1996 |
| rx00873 | 779 | GB_BA1:SCO001206 | 9184 | AJ001206 | Streptomyces coelicolor A3(2), glycogen metabolism cluster II. | 63,415 | 29-MAR-1999 |
| | | GB_BA1:SCO001205 | 9589 | AJ001205 | Streptomyces coelicolor A3(2) glycogen metabolism clusterI. | 61,617 | 29-MAR-1999 |

TABLE 4: ALIGNMENT RESULTS

| Accession | Gene ID | Gene Name | Protein Name | Function | Source | Date |
|-----------|---------|---|--|--|---|--|
| rx00884 | 1263 | GB_BA1:D78198 GB_BA1:MTCY253 GB_BA1:MSGY222 GB_GSS15:AQ654600 | 2304 41230 41156 468 | D78198 Z81368 AD000010 AQ654600 | Pimelobacter sp. DNA for trehalose synthase, complete cds. Mycobacterium tuberculosis H37Rv complete genome; segment 106/162. Mycobacterium tuberculosis sequence from clone y222. Sheared DNA-1O14:TF Sheared DNA Trypanosoma brucei genomic clone | 5-Feb-99 17-Jun-98 03-DEC-1996 22-Jun-99 |
| rx00891 | 1102 | GB_BA1:MTCI418B GB_BA1:SCO001206 GB_BA1:SCO001205 EM_PAT:E10963 | 11700 9184 9589 3118 | Z96071 AJ001206 AJ001205 E10963 | Sheared DNA-1O14, genomic survey sequence. Mycobacterium tuberculosis H37Rv complete genome; segment 7/162. Streptomyces coelicolor A3(2), glycogen metabolism cluster II. Streptomyces coelicolor A3(2) glycogen metabolism cluster gDNA encoding tryptophan synthase. | 18-Jun-98 29-MAR-1999 29-MAR-1999 08-OCT-1997 (Rel. 52, Created) |
| rx00952 | 963 | | | | | |
| rx00954 | 644 | GB_BA1:BLTRP GB_PAT:E01688 GB_PAT:E01375 GB_PAT:E01688 GB_BA1:BLTRP GB_PAT:E01375 GB_PAT:BLTRP GB_PAT:E01688 GB_PAT:E01688 EM_PAT:E10963 | 7725 7725 7726 7725 7725 7726 7725 7725 7725 3118 | X04960 E01688 E01375 E01688 X04960 E01375 X04960 E01688 E10963 | Brevibacterium lactofermentum tryptophan operon. Genomic DNA of trp operon of prepilactrium latophilmentam. DNA sequence of tryptophan operon. Genomic DNA of trp operon of prepilactrium latophilmentam. Brevibacterium lactofermentum tryptophan operon. DNA sequence of tryptophan operon. Brevibacterium lactofermentum tryptophan operon. Genomic DNA of trp operon of prepilactrium latophilmentam. gDNA encoding tryptophan synthase. | 10-Feb-99 29-Sep-97 29-Sep-97 29-Sep-97 10-Feb-99 29-Sep-97 10-Feb-99 29-Sep-97 08-OCT-1997 (Rel. 52, Created) |
| rx00955 | 1545 | | | | | |
| rx00956 | 1237 | | | | | |
| rx00957 | 1677 | GB_BA1:BLTRP GB_PAT:E01375 GB_BA1:BLTRP GB_PAT:E01375 GB_PAT:E01688 GB_BA1:BLTRP GB_PAT:E01375 GB_PAT:E01688 GB_BA1:CGHOMTHR | 7725 7726 7725 7726 7725 7725 7726 7725 7725 3685 | X04960 E01375 X04960 E01375 E01688 X04960 E01375 E01688 Y00546 | Brevibacterium lactofermentum tryptophan operon. DNA sequence of tryptophan operon. Brevibacterium lactofermentum tryptophan operon. DNA sequence of tryptophan operon. Genomic DNA of trp operon of prepilactrium latophilmentam. Brevibacterium lactofermentum tryptophan operon. DNA sequence of tryptophan operon. Genomic DNA of trp operon of prepilactrium latophilmentam. Corynebacterium glutamicum hom-thrB genes for homoserine dehydrogenase and homoserine kinase. | 10-Feb-99 29-Sep-97 10-Feb-99 29-Sep-97 29-Sep-97 10-Feb-99 29-Sep-97 29-Sep-97 12-Sep-93 |
| rx00970 | 1050 | GB_PAT:109077 GB_PAT:E01358 | 3685 2615 | I09077 E01358 | Sequence 1 from Patent WO 8809819. DNA encoding for homoserine dehydrogenase(HDH)and homoserine kinase(HK). | 02-DEC-1994 29-Sep-97 |
| rx00972 | 1458 | GB_PAT:E16755 | 3579 | E16755 | gDNA encoding diaminopimelate decarboxylase (DDC) and arginyl-tRNA synthase. | 28-Jul-99 |
| rx00981 | 753 | GB_PAT:AR038110 GB_PAT:E14508 GB_OV:GGA245664 GB_PL2:AC007887 | 3579 3579 512 159434 | AR038110 E14508 AJ245664 AC007887 | Sequence 15 from patent US 5804414. DNA encoding Brevibacterium diaminopimelic acid decarboxylase and arginyl-tRNA synthase. Gallus gallus partial mRNA for ATP-citrate lyase (ACL gene). Genomic sequence for Arabidopsis thaliana BAC F15O4 from chromosome I, complete sequence. | 29-Sep-99 28-Jul-99 28-Sep-99 04-OCT-1999 |

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TABLE 4: ALIGNMENT RESULTS

| | GB_GSS1:CNS00RNW 542 | AL087338 | Arabidopsis thaliana genome survey sequence T7 end of BAC F14D7 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence. | 41,264 | 28-Jun-99 |
|--------------|-------------------------|----------|---|---------|-------------|
| rx00989 1644 | GB_BA1:MTV008 63033 | AL021246 | Mycobacterium tuberculosis H37Rv complete genome, segment 108/162. | 40,773 | 17-Jun-98 |
| | GB_BA1:SCVALSFP 3619 | Y13070 | S.coelicolor valS, fpgs, ndk genes. | 58,119 | 03-MAR-1998 |
| | GB_BA1:MTV008 63033 | AL021246 | Mycobacterium tuberculosis H37Rv complete genome, segment 108/162. | 38,167 | 17-Jun-98 |
| rx00997 705 | GB_BA2:CGU31225 1817 | U31225 | Corynebacterium glutamicum L-proline:NADP+ 5-oxido-reductase (proC) gene, complete cds. | 40,841 | 2-Aug-96 |
| | GB_HTG1:CEY39C12 282838 | AL009026 | Caenorhabditis elegans chromosome IV clone Y39C12, *** SEQUENCING IN PROGRESS ***, in unordered pieces. | 36,416 | 26-OCT-1999 |
| | GB_IN1:CEB0001 39416 | Z69634 | Caenorhabditis elegans cosmid B0001, complete sequence. | 36,416 | 2-Sep-99 |
| rx01019 1110 | GB_HTG2:AC005052 144734 | AC005052 | Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces. | 39,172 | 12-Jun-98 |
| | GB_HTG2:AC005052 144734 | AC005052 | Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces. | 39,172 | 12-Jun-98 |
| | GB_GSS9:QA171808 512 | AQ171808 | HS_3179_A1_G03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3179 Col=5 Row=M, genomic survey sequence. | 34,661 | 17-OCT-1998 |
| rx01026 1782 | GB_BA1:SC1C2 42210 | AL031124 | Streptomyces coelicolor cosmid 1C2. | 68,275 | 15-Jan-99 |
| | GB_BA1:ATLEUCD 2982 | X84647 | A.teichomyceticus leuC and leuD genes. | 65,935 | 04-OCT-1995 |
| rx01027 1131 | GB_BA1:MTV012 70287 | AL021287 | Mycobacterium tuberculosis H37Rv complete genome, segment 132/162. | 40,454 | 23-Jun-99 |
| | GB_BA1:MLCB637 44882 | Z99263 | Mycobacterium leprae cosmid B637. | 38,636 | 17-Sep-97 |
| | GB_BA1:MTCY349 43523 | Z83018 | Mycobacterium tuberculosis H37Rv complete genome, segment 131/162. | 51,989 | 17-Jun-98 |
| | GB_BA1:SPUNGMTX 1172 | Z21702 | S.pneumoniae ung gene and muX genes encoding uracil-DNA glycosylase and 8-oxodGTP nucleoside triphosphatase. | 38,088 | 15-Jun-94 |
| rx01073 954 | GB_BA1:BACOUTB 1004 | M15811 | Bacillus subtilis outB gene encoding a sporulation protein, complete cds. | 53,723 | 26-Apr-93 |
| | GB_PR4:AC007938 167237 | AC007938 | Homo sapiens clone UWGC-djs201 from 7q31, complete sequence. | 34,322 | 1-Jul-99 |
| | GB_PL2:ATAC006282 92577 | AC006282 | Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete Arabidopsis thaliana sequence. | 36,181 | 13-MAR-1999 |
| rx01079 2226 | GB_BA2:AF112535 4363 | AF112535 | Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds. | 99,820 | 5-Aug-99 |
| | GB_BA1:CANRDFGEN 6054 | Y09572 | Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes. | 75,966 | 18-Apr-98 |
| rx01080 567 | GB_BA1:MTV012 70287 | AL021287 | Mycobacterium tuberculosis H37Rv complete genome, segment 132/162. | 38,296 | 23-Jun-99 |
| | GB_BA2:AF112535 4363 | AF112535 | Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds. | 100,000 | 5-Aug-99 |
| | GB_BA1:CANRDFGEN 6054 | Y09572 | Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes. | 65,511 | 18-Apr-98 |
| rx01087 999 | GB_BA1:STNRD 4894 | X73226 | S.typhimurium nrdEF operon. | 52,477 | 03-MAR-1997 |
| | GB_IN2:AF063412 1093 | AF063412 | Limnadia lenticularis elongation factor 1-alpha mRNA, partial cds. | 43,750 | 29-MAR-1999 |
| | GB_PR3:HS24M15 134539 | Z94055 | Human DNA sequence from PAC 24M15 on chromosome 1. Contains tenascin-R (restictin), EST. | 37,475 | 23-Nov-99 |
| | GB_IN2:ARU85702 1240 | U85702 | Anathix ralla elongation factor-1 alpha (EF-1a) gene, partial cds. | 37,319 | 16-Jul-97 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|--|---|--|---|---|--|--|
| rx01095 | 857 | GB_BA1:MTCY01B2 GB_HTG5:AC011632 | 35938 175917 | Z95554 AC011632 | Mycobacterium tuberculosis H37Rv complete genome; segment 72/162. Homo sapiens clone RP11-3N13, WORKING DRAFT SEQUENCE, 9 unordered pieces. Homo sapiens clone RP11-3N13, WORKING DRAFT SEQUENCE, 9 unordered pieces. Corynebacterium glutamicum cyclase (hisF) gene, complete cds. Corynebacterium glutamicum cyclase (hisF) gene, complete cds. | Mycobacterium tuberculosis Homo sapiens Homo sapiens Corynebacterium glutamicum Corynebacterium glutamicum | 43,243 36,471 36,836 100,000 41,206 | 17-Jun-98 19-Nov-99 19-Nov-99 13-Nov-97 13-Nov-97 |
| rx01097 | 477 | GB_BA2:AF030405 GB_BA2:AF030405 | 774 774 | AF030405 AF030405 | Corynebacterium glutamicum cyclase (hisF) gene, complete cds. Corynebacterium leprae cosmid B1610. Corynebacterium glutamicum phosphoribosylformimino-5-amino-1- phosphoribosyl-4-imidazolecarboxamide isomerase (hisA) gene, complete cds. | Corynebacterium glutamicum Mycobacterium tuberculosis Mycobacterium leprae Corynebacterium glutamicum | 97,933 40,972 61,366 97,154 | 13-Nov-97 10-DEC-1996 27-Aug-99 12-MAR-1998 |
| rx01098 | 897 | GB_BA2:AF030405 GB_BA1:MSGY223 GB_BA1:MLCB1610 GB_BA2:AF051846 | 774 42061 40055 738 | AF030405 AD000019 AL049913 AF051846 | Corynebacterium glutamicum cyclase (hisF) gene, complete cds Mycobacterium tuberculosis sequence from clone y223. Corynebacterium leprae cosmid B1610. Corynebacterium glutamicum phosphoribosylformimino-5-amino-1- phosphoribosyl-4-imidazolecarboxamide isomerase (hisA) gene, complete cds. | Corynebacterium glutamicum Mycobacterium tuberculosis Mycobacterium leprae Corynebacterium glutamicum | 97,933 40,972 61,366 97,154 | 13-Nov-97 10-DEC-1996 27-Aug-99 12-MAR-1998 |
| rx01100 | 861 | GB_BA2:AF060558 | 636 | AF060558 | Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds. | Corynebacterium glutamicum | 95,455 | 29-Apr-98 |
| rx01101 | 756 | GB_HTG1:HSDJ140A9 GB_BA2:AF060558 GB_BA1:SC4G6 GB_BA1:STMHISOPA GB_BA1:STMHISOPA GB_BA1:SC4G6 | 221755 636 36917 3981 3981 36917 | AL109917 AF060558 AL096884 M31628 M31628 AL096884 | Homo sapiens chromosome 1 clone RP1-140A9, *** SEQUENCING IN PROGRESS ***, in unordered pieces. Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds. Streptomyces coelicolor cosmid 4G6. S.coelicolor histidine biosynthesis operon encoding hisD, partial cds., and hisC, hisB, hisH, and hisA genes, complete cds. S.coelicolor histidine biosynthesis operon encoding hisD, partial cds , and hisC, hisB, hisH, and hisA genes, complete cds. Streptomyces coelicolor cosmid 4G6. | Homo sapiens Corynebacterium glutamicum Streptomyces coelicolor Streptomyces coelicolor Streptomyces coelicolor A3(2) Streptomyces coelicolor Streptomyces coelicolor A3(2) | 30,523 94,462 38,378 60,053 58,333 39,045 | 23-Nov-99 29-Apr-98 23-Jul-99 26-Apr-93 26-Apr-93 23-Jul-99 |
| rx01105 | 1221 | GB_BA1:MTCY336 GB_BA1:MTCY336 GB_BA1:MSGY223 GB_BA1:MLCB1610 GB_BA1:MSGY223 GB_BA1:MSHISCD | 32437 32437 42061 40055 42061 2298 | Z95586 Z95586 AD000019 AL049913 AD000019 X65542 | Mycobacterium tuberculosis H37Rv complete genome, segment 70/162. Mycobacterium tuberculosis H37Rv complete genome, segment 70/162. Mycobacterium tuberculosis sequence from clone y223. Mycobacterium leprae cosmid B1610. Mycobacterium tuberculosis sequence from clone y223. M. smegmatis genes hisD and hisC for histidinol dehydrogenase and histidinol- phosphate aminotransferase, respectively. | Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium leprae Mycobacterium tuberculosis Mycobacterium tuberculosis | 60,364 60,931 36,851 60,902 37,233 60,111 | 24-Jun-99 24-Jun-99 10-DEC-1996 27-Aug-99 10-DEC-1996 30-Jun-93 |
| rx01145 | 1137 | GB_BA1:MTCY336 GB_BA1:CORAIA GB_BA1:BRILVCA | 32437 4705 1364 | Z95586 L09232 D14551 | Mycobacterium tuberculosis H37Rv complete genome, segment 70/162. Corynebacterium glutamicum acetoaldehyde acid synthase (ilvB) and (ilvN) genes, and acetoaldehyde acid isomerase (ilvC) gene, complete cds. Brevibacterium flavum ilvC gene for acetoaldehyde acid isomerase, complete cds. | Mycobacterium tuberculosis Corynebacterium glutamicum Corynebacterium glutamicum | 58,420 100,000 99,560 | 24-Jun-99 23-Feb-95 3-Feb-99 |
| rx01162 | 1449 | GB_PAT_E08232 GB_PAT_A60299 GB_PR3_HS24E5 | 1017 2869 35506 | E08232 A60299 Z82185 | DNA encoding acetoaldehyde-acid isomerase reductase. Sequence 18 from Patent WO9706281. Human DNA sequence from Fosmid 24E5 on chromosome 22q11.2-qter contains parvalbumin, ESTs, STS. | Corynebacterium glutamicum Aspergillus niger Homo sapiens | 99,803 38,675 36,204 | 29-Sep-97 06-MAR-1998 23-Nov-99 |

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TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|----------|------|-------------------|--------|----------|---|----------------------------|--------|-------------|
| rxa01208 | 846 | GB_PR3:AC005265 | 43900 | AC005265 | Homo sapiens chromosome 19, cosmid F19750, complete sequence. | Homo sapiens | 38,363 | 6-Jul-98 |
| | | GB_HTG2:AC004965 | 323792 | AC004965 | Homo sapiens clone DJ1106H14, *** SEQUENCING IN PROGRESS ***; 42 unordered pieces. | Homo sapiens | 36,058 | 12-Jun-98 |
| | | GB_HTG2:AC004965 | 323792 | AC004965 | Homo sapiens clone DJ1106H14, *** SEQUENCING IN PROGRESS ***; 42 unordered pieces. | Homo sapiens | 36,058 | 12-Jun-98 |
| | | GB_PL2:TAU55859 | 2397 | U55859 | Triticum aestivum heat shock protein 80 mRNA, complete cds. | Triticum aestivum | 37,269 | 1-Feb-99 |
| rxa01209 | 1528 | GB_HTG3:AC011469 | 113436 | AC011469 | Homo sapiens chromosome 19 clone CIT-HSPC_475D23, *** SEQUENCING IN PROGRESS ***; 31 unordered pieces. | Homo sapiens | 40,000 | 07-OCT-1999 |
| | | GB_HTG3:AC011469 | 113436 | AC011469 | Homo sapiens chromosome 19 clone CIT-HSPC_475D23, *** SEQUENCING IN PROGRESS ***; 31 unordered pieces. | Homo sapiens | 40,000 | 07-OCT-1999 |
| | | GB_PL1:AB010077 | 77380 | AB010077 | Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence. | Arabidopsis thaliana | 36,803 | 20-Nov-99 |
| rxa01215 | 1098 | GB_BA1:MTCY10G2 | 38970 | Z92539 | Mycobacterium tuberculosis H37Rv complete genome; segment 47/162. | Mycobacterium tuberculosis | 37,047 | 17-Jun-98 |
| | | GB_IN1:LEIPRP | 1887 | M76553 | Leishmania donovani phosphoribosylpyrophosphate synthetase gene, complete cds. | Leishmania donovani | 50,738 | 7-Jun-93 |
| | | GB_HTG2:HSJ799D16 | 130149 | AL050344 | Homo sapiens chromosome 1 clone RP4-799D16 map p34.3-36.1, *** SEQUENCING IN PROGRESS ***; in unordered pieces. | Homo sapiens | 38,135 | 29-Nov-99 |
| rxa01239 | 2556 | GB_BA1:MTCY48 | 35377 | Z74020 | Mycobacterium tuberculosis H37Rv complete genome; segment 69/162. | Mycobacterium tuberculosis | 38,139 | 17-Jun-98 |
| | | GB_PR2:AB029032 | 6377 | AB029032 | Homo sapiens mRNA for KIAA1109 protein, partial cds. | Homo sapiens | 39,394 | 4-Aug-99 |
| | | GB_GSS9:AQ107201 | 355 | AQ107201 | HS_3098_A1_C03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3098 Col=5 Row=E, genomic survey sequence. | Homo sapiens | 41,408 | 28-Aug-98 |
| rxa01253 | 873 | GB_PL2:F5O8 | 99923 | AC005990 | Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence. | Arabidopsis thaliana | 36,118 | 23-DEC-1998 |
| | | GB_PL2:F5O8 | 99923 | AC005990 | Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence. | Arabidopsis thaliana | 35,574 | 23-DEC-1998 |
| rxa01321 | 1044 | GB_IN1:CELC06G1 | 31205 | U41014 | Caenorhabditis elegans cosmid C06G1. | Caenorhabditis elegans | 38,560 | 30-Nov-95 |
| | | GB_GSS14:AQ518843 | 441 | AQ518843 | HS_5106_A1_D10_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=682 Col=19 Row=G, genomic survey sequence | Homo sapiens | 41,121 | 05-MAY-1999 |
| | | GB_HTG2:AC007473 | 194859 | AC007473 | Drosophila melanogaster chromosome 2 clone BACR38D12 (D590) RPCI-98 38.D.12 map 48A-48B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 60 unordered pieces. | Drosophila melanogaster | 40,634 | 2-Aug-99 |
| | | GB_HTG4:AC011696 | 115847 | AC011696 | Drosophila melanogaster chromosome 2 clone BACR35F01 (D1156) RPCI-98 35.F.1 map 48A-48C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 108 unordered pieces. | Drosophila melanogaster | 38,290 | 26-OCT-1999 |
| rxa01352 | 706 | GB_PL2:ATAC005167 | 83260 | AC005167 | Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence. | Arabidopsis thaliana | 34,311 | 15-OCT-1998 |
| | | GB_PL2:ATAC005825 | 97380 | AC005825 | Arabidopsis thaliana chromosome II BAC T24121 genomic sequence, complete sequence. | Arabidopsis thaliana | 34,311 | 12-Apr-99 |
| | | GB_HTG3:AC011150 | 127222 | AC011150 | Homo sapiens clone 4_K_17, LOW-PASS SEQUENCE SAMPLING. | Homo sapiens | 37,722 | 01-OCT-1999 |
| rxa01360 | 259 | GB_EST32:A1725583 | 728 | A1725583 | BNLGH112371 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (U86081) root hair defective 3 [Arabidopsis thaliana], mRNA sequence. | Gossypium hirsutum | 38,492 | 11-Jun-99 |
| | | GB_PR2:HS227P17 | 82951 | Z81007 | Human DNA sequence from PAC 227P17, between markers DXS6791 and DXS8038 on chromosome X contains CpG island. EST. | Homo sapiens | 39,738 | 23-Nov-99 |

TABLE 4: ALIGNMENT RESULTS

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|---------|------|-------------------|--------|----------|--|------------------------------|---------|-------------|
| rx01361 | 629 | GB_EST34:AV171099 | 173 | AV171099 | AV171099 Mus musculus head C57BL/6J 14, 17 day embryo Mus musculus cDNA clone 320002M11, mRNA sequence. | Mus musculus | 46,237 | 6-Jul-99 |
| | | GB_RO:AB008915S1 | 530 | AB008915 | Mus musculus mGpi1 gene, exon 1. | Mus musculus | 45,574 | 28-Sep-99 |
| | | GB_EST22:AI050532 | 293 | AI050532 | uc83d10.y1 Sugano mouse kidney mika Mus musculus cDNA clone IMAGE:1432243 5' similar to TR:O35120 O35120 MGPI1P. ; mRNA sequence. | Mus musculus | 44,097 | 9-Jul-98 |
| rx01381 | 944 | GB_RO:AB008895 | 3062 | AB008895 | Mus musculus mRNA for mGpi1p, complete cds. | Mus musculus | 41,316 | 23-Nov-97 |
| | | GB_PL1:AB005237 | 87835 | AB005237 | Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence. | Arabidopsis thaliana | 36,606 | 20-Nov-99 |
| | | GB_GSS5:AQ766840 | 491 | AQ766840 | HS_2026_A2_C09_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=18 Row=E, genomic survey sequence. | Homo sapiens | 37,916 | 28-Jul-99 |
| rx01393 | 993 | GB_BA1:MTV043 | 68848 | AL022004 | Mycobacterium tuberculosis H37Rv complete genome, segment 40/162. | Mycobacterium tuberculosis | 37,419 | 24-Jun-99 |
| | | GB_BA1:CGLYSEG | 2374 | X96471 | C.glutamicum lysE and lysG genes. | Corynebacterium glutamicum | 34,831 | 24-Feb-97 |
| | | GB_BA1:SC5A7 | 40337 | AL031107 | Streptomyces coelicolor cosmid SA7. | Streptomyces coelicolor | 35,138 | 27-Jul-98 |
| | | GB_FR3:AC004054 | 112184 | AC004054 | Homo sapiens chromosome 4 clone B220G8 map 4q21, complete sequence. | Homo sapiens | 37,277 | 9-Jul-98 |
| rx01394 | 822 | GB_BA1:CGLYSEG | 2374 | X96471 | C.glutamicum lysE and lysG genes. | Corynebacterium glutamicum | 100,000 | 24-Feb-97 |
| | | GB_GSS5:AQ769223 | 500 | AQ769223 | HS_3155_B2_G10_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3155 Col=20 Row=N, genomic survey sequence. | Homo sapiens | 38,400 | 28-Jul-99 |
| rx01416 | 630 | GB_BA1:CGLYSEG | 2374 | X96471 | C.glutamicum lysE and lysG genes. | Corynebacterium glutamicum | 33,665 | 24-Feb-97 |
| | | GB_BA1:SC3C3 | 31382 | AL031231 | Streptomyces coelicolor cosmid 3C3. | Streptomyces coelicolor | 62,726 | 10-Aug-98 |
| | | GB_BA1:MLCB22 | 40281 | Z98741 | Mycobacterium leprae cosmid B22. | Mycobacterium leprae | 39,159 | 22-Aug-97 |
| rx01442 | 1347 | GB_BA1:MTV002 | 56414 | AL008967 | Mycobacterium tuberculosis H37Rv complete genome; segment 122/162. | Mycobacterium tuberculosis | 37,340 | 17-Jun-98 |
| | | GB_BA1:D90827 | 18886 | D90827 | E.coli genomic DNA, Kohara clone #336(41.2-41.5 min.). | Escherichia coli | 58,517 | 21-MAR-1997 |
| | | GB_BA1:D90828 | 14590 | D90828 | E.coli genomic DNA, Kohara clone #336gap(41.6-41.9 min.). | Escherichia coli | 56,151 | 21-MAR-1997 |
| rx01446 | 1413 | GB_BA2:AE000279 | 10855 | AE000279 | Escherichia coli K-12 MG1655 section 169 of 400 of the complete genome. | Escherichia coli | 56,021 | 12-Nov-98 |
| | | GB_BA1:SCH10 | 39524 | AL049754 | Streptomyces coelicolor cosmid H10. | Streptomyces coelicolor | 39,037 | 04-MAY-1999 |
| | | GB_BA1:MTY13E10 | 35019 | Z95324 | Mycobacterium tuberculosis H37Rv complete genome; segment 18/162. | Mycobacterium tuberculosis | 40,130 | 17-Jun-98 |
| | | GB_BA1:MLCB4 | 36310 | AL023514 | Mycobacterium leprae cosmid B4. | Mycobacterium leprae | 37,752 | 27-Aug-99 |
| rx01483 | 1395 | GB_BA1:MTCY98 | 31225 | Z83860 | Mycobacterium tuberculosis H37Rv complete genome; segment 103/162. | Mycobacterium tuberculosis | 39,057 | 17-Jun-98 |
| | | GB_BA1:MSG81229CS | 30670 | L78812 | Mycobacterium leprae cosmid B1229 DNA sequence. | Mycobacterium leprae | 54,382 | 15-Jun-96 |
| | | GB_BA2:AF027507 | 5168 | AF027507 | Mycobacterium smegmatis dGTPase (dgt), and primase (dnaG) genes, complete cds; tRNA-Asn gene, complete sequence. | Mycobacterium smegmatis | 52,941 | 16-Jan-98 |
| rx01486 | 757 | GB_BA1:MTV002 | 56414 | AL008967 | Mycobacterium tuberculosis H37Rv complete genome; segment 122/162. | Mycobacterium tuberculosis | 40,941 | 17-Jun-98 |
| | | GB_BA1:MLCB22 | 40281 | Z98741 | Mycobacterium leprae cosmid B22. | Mycobacterium leprae | 38,451 | 22-Aug-97 |
| | | GB_BA1:SC3C3 | 31382 | AL031231 | Streptomyces coelicolor cosmid 3C3. | Streptomyces coelicolor | 61,194 | 10-Aug-98 |
| rx01489 | 1146 | GB_BA1:CORFADS | 1547 | D37967 | Corynebacterium ammoniagenes gene for FAD synthetase, complete cds | Corynebacterium ammoniagenes | 58,021 | 8-Feb-99 |
| | | GB_BA1:MLCB22 | 40281 | Z98741 | Mycobacterium leprae cosmid B22. | Mycobacterium leprae | 38,414 | 22-Aug-97 |
| | | GB_BA1:SC10A7 | 39739 | AL078618 | Streptomyces coelicolor cosmid 10A7. | Streptomyces coelicolor | 36,930 | 9-Jun-99 |
| rx01491 | 774 | GB_BA1:MTV002 | 56414 | AL008967 | Mycobacterium tuberculosis H37Rv complete genome; segment 122/162. | Mycobacterium tuberculosis | 37,062 | 17-Jun-98 |

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TABLE 4: ALIGNMENT RESULTS

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|----------|------|--|---|--|---|---|--|---|
| rxa01508 | 1662 | GB_EST13:AA356956 GB_OV:OMDNAPROI GB_IN1:CEF28C12 GB_IN1:CEF28C12 | 255 7327 14653 14653 | AA356956 X92380 Z93380 Z93380 | EST5614 Jurkat T-cells III Homo sapiens cDNA 5' end, mRNA sequence. O.mossambicus prolactin I gene. Caenorhabditis elegans cosmid F28C12, complete sequence. Caenorhabditis elegans cosmid F28C12, complete sequence. | Homo sapiens Tilapia mossambica Caenorhabditis elegans Caenorhabditis elegans | 37,647 38,289 37,984 38,469 | 21-Apr-97 19-OCT-1995 23-Nov-98 23-Nov-98 |
| rx01512 | 723 | GB_BA1:SC59 GB_BA1:MAU88875 | 37730 840 | AL049841 U88875 | Streptomyces coelicolor cosmid E9. Mycobacterium avium hypoxanthine-guanine phosphoribosyl transferase gene. Mycobacterium avium complete cds. | Streptomyces coelicolor Mycobacterium avium | 39,021 57,521 | 19-MAY-1999 05-MAR-1997 |
| rx01514 | 711 | GB_BA1:MTY15C10 GB_BA1:MTCY7H7B GB_BA1:MLCB2548 GB_PL1:EGGTPCHI GB_PL1:ECOUW93 GB_BA1:ECOUW93 GB_BA1:MTCY49 GB_IN1:DMEZ38847 | 33050 24244 38916 242 338534 338534 39430 5419 | Z95436 Z95557 AL023093 Z49757 U14003 U14003 Z73966 AJ238847 | Mycobacterium tuberculosis H37Rv complete genome; segment 154/162. Mycobacterium tuberculosis H37Rv complete genome; segment 153/162. Mycobacterium leprae cosmid B2548. E.gracilis mRNA for GTP cyclohydrolase I (core region). Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes. Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes. Mycobacterium tuberculosis H37Rv complete genome; segment 93/162. Drosophila melanogaster mRNA for drosophila dodeca-satellite protein 1 (DDP-Drosophila melanogaster 1). | Mycobacterium tuberculosis Mycobacterium tuberculosis Mycobacterium leprae Euglena gracilis Escherichia coli Escherichia coli Mycobacterium tuberculosis Drosophila melanogaster | 40,086 43,343 38,177 64,876 38,943 37,500 38,010 36,346 | 17-Jun-98 18-Jun-98 27-Aug-99 20-OCT-1995 17-Apr-96 17-Apr-96 24-Jun-99 13-Aug-99 |
| rx01516 | 513 | GB_HTG3:AC009210 | 103814 | AC009210 | Drosophila melanogaster chromosome 2 clone BACR01106 (D1054) RPCI-98 01.1.6 map 55D-55D strain y; on bw sp. *** SEQUENCING IN PROGRESS ***, 86 unordered pieces. | Drosophila melanogaster | 37,897 | 20-Aug-99 |
| rx01517 | 600 | GB_IN2:AF132179 GB_PL2:F6H8 GB_PL2:AF038831 | 4842 82596 647 | AF132179 AF178045 AF038831 | Drosophila melanogaster clone LD21677 unknown mRNA. Arabidopsis thaliana BAC F6H8. Sorosporium saponariae internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence. | Drosophila melanogaster Arabidopsis thaliana Sorosporium saponariae | 36,149 35,846 40,566 | 3-Jun-99 19-Aug-99 13-Apr-99 |
| rx01528 | 651 | GB_PL2:ATAC005957 GB_BA1:ANANIFBH GB_PR2:AC002461 GB_PR2:AC002461 GB_RO:MM437P9 GB_PR3:AC005740 | 108355 5936 197273 197273 165901 186780 | AC005957 J05111 AC002461 AC002461 AL049866 AC005740 | Arabidopsis thaliana chromosome II BAC T15J14 genomic sequence, complete sequence. Anabaena sp. (clone AnH20.1) nitrogen fixation operon nifB, fixN, nifS, nifU, and nifH genes, complete cds. Human BAC clone RG204116 from 7q31, complete sequence. Human BAC clone RG204116 from 7q31, complete sequence. Mus musculus chromosome X, clone 437P9. Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence. | Arabidopsis thaliana Anabaena sp. Homo sapiens Homo sapiens Mus musculus Homo sapiens | 38,095 38,206 36,623 34,719 37,500 37,031 | 7-Jan-99 26-Apr-93 20-Aug-97 20-Aug-97 29-Jun-99 01-OCT-1998 |
| rx01551 | 1998 | GB_PR3:AC005740 GB_BA1:MTCY22G10 GB_BA2:ECOUW89 GB_BA1:SCQ11 GB_IN1:CEY62H9A GB_PR4:HSU51003 GB_OM:PIGDAO1 GB_BA1:MTCI125 GB_BA1:U00021 GB_BA1:MLCB1351 | 186780 35420 176195 15441 47396 3202 395 37432 39193 38936 | AC005740 Z84724 U00006 AL096823 AL032630 U51003 M18444 Z98268 U00021 Z95117 | Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence. Mycobacterium tuberculosis H37Rv complete genome; segment 21/162. E. coli chromosomal region from 89.2 to 92.8 minutes. Streptomyces coelicolor cosmid Q11. Caenorhabditis elegans cosmid Y62H9A, complete sequence. Homo sapiens DLX-2 (DLX-2) gene, complete cds. Pig D-amino acid oxidase (DAO) gene, exon 1. Mycobacterium tuberculosis H37Rv complete genome; segment 76/162. Mycobacterium leprae cosmid L247. Mycobacterium leprae cosmid B1351. | Mycobacterium tuberculosis Escherichia coli Streptomyces coelicolor Caenorhabditis elegans Homo sapiens Sus scrofa Mycobacterium tuberculosis Mycobacterium leprae Mycobacterium leprae | 38,371 38,064 60,775 38,514 37,730 39,340 63,300 36,756 36,756 | 17-Jun-98 17-DEC-1993 8-Jul-99 2-Sep-99 07-DEC-1999 27-Apr-93 17-Jun-98 29-Sep-94 24-Jun-97 |

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TABLE 4: ALIGNMENT RESULTS

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|---------|------|---|--------------------------------------|--|---|---|---|---|
| rx01617 | 795 | GB_PR2:HSMTM0 | 217657 | AL034384 | Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100; complete sequence bases 1..217657. | Homo sapiens | 40,811 | 5-Jul-99 |
| | | GB_PR2:HS13D10 | 153147 | AL021407 | Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island. | Homo sapiens | 38,768 | 23-Nov-99 |
| | | GB_PR2:HSMTM0 | 217657 | AL034384 | Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100; complete sequence bases 1..217657. | Homo sapiens | 39,018 | 5-Jul-99 |
| rx01657 | 723 | GB_BA1:MTCY1A10 GB_EST6:D79278 | 25949 392 | Z95387 D79278 | Mycobacterium tuberculosis H37Rv complete genome; segment 117/162. HUM213D06B Human aorta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-213D06 5', mRNA sequence. | Mycobacterium tuberculosis Homo sapiens | 40,656 44,262 | 17-Jun-98 9-Feb-96 |
| | | GB_BA2:AF129925 GB_BA1:MTV013 GB_RO:MMFV1 | 10243 11364 6480 | AF129925 AL021309 X97719 | Thiobacillus ferrooxidans carboxysome operon, complete cds. Mycobacterium tuberculosis H37Rv complete genome; segment 134/162. Mus musculus retrovirus restriction gene Fv1. | Thiobacillus ferrooxidans Mycobacterium tuberculosis Mus musculus | 40,709 40,986 35,364 | 17-MAY-1999 17-Jun-98 29-Aug-96 |
| | | GB_PAT:A67508 GB_VI:TVU95309 GB_VI:TVU95303 GB_VI:TVU95302 GB_EST5:H91843 | 6480 600 600 600 362 | A67508 U95309 U95302 U95303 H91843 | Sequence 1 from Patent WO9743410. Tula virus O64 nucleocapsid protein gene, partial cds. Tula virus O52 nucleocapsid protein gene, partial cds. Tula virus O24 nucleocapsid protein gene, partial cds. ys81e01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:221208 Homo sapiens 3' similar to gb-X63749_rna1 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-1 (HUMAN); mRNA sequence human STS SHGC-30023, sequence tagged site. | Tula virus Tula virus Tula virus Homo sapiens | 35,364 41,894 41,712 39,576 39,157 | 05-MAY-1999 28-OCT-1997 28-OCT-1997 28-OCT-1997 29-Nov-95 |
| rx01660 | 675 | GB_STG:G26925 GB_PL2:AF139451 GB_BA1:SC1C2 GB_EST22:A1064232 | 362 1202 42210 493 | G26925 AF139451 AL031124 A1064232 | Gossypium robinsonii Cella2 pseudogene, partial sequence. Streptomyces coelicolor cosmid 1C2. GH04563.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH04563 5prime, mRNA sequence. | Homo sapiens Gossypium robinsonii Streptomyces coelicolor Drosophila melanogaster | 39,157 38,910 60,644 38,037 | 14-Jun-96 1-Jun-99 15-Jan-99 24-Nov-98 |
| rx01692 | 873 | GB_IN2:AF117896 GB_BA2:AF067123 GB_RO:RATNFHPEP GB_RO:RSNFH GB_BA2:AF124600 | 1020 1034 3085 3085 4115 | AF117896 AF067123 M37227 X13804 AF124600 | Drosophila melanogaster neuropeptide F (npf) gene, complete cds. Lactobacillus reuteri cobalamin biosynthesis protein J (cbuJ) gene, partial cds, and uroporphyrin-III C-methyltransferase (sumT) gene, complete cds. Rat heavy neurofilament (NF-H) polypeptide, partial cds. Rat mRNA for heavy neurofilament polypeptide NF-H C-terminus. Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinate synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepQ) gene, partial cds. | Drosophila melanogaster Lactobacillus reuteri Rattus norvegicus Rattus sp. Corynebacterium glutamicum | 36,122 48,079 37,093 37,093 100,000 | 2-Jul-99 3-Jun-98 27-Apr-93 14-Jul-95 04-MAY-1999 |
| rx01698 | 1353 | GB_BA1:MTCY159 GB_BA1:MSGB937CS GB_BA2:AF124600 | 33818 38914 4115 | Z83863 L78820 AF124600 | Mycobacterium tuberculosis H37Rv complete genome; segment 111/162. Mycobacterium leprae cosmid B937 DNA sequence. Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinate synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepQ) gene, partial cds. | Mycobacterium tuberculosis Mycobacterium leprae Corynebacterium glutamicum | 36,323 62,780 100,000 | 17-Jun-98 15-Jun-96 04-MAY-1999 |
| | | GB_BA2:AF016585 | 41097 | AF016585 | Streptomyces caelestis cytochrome P-450 hydroxylase homolog (nidi) gene, partial cds; polyketide synthase modules 1 through 7 (nida) genes, complete cds; and N-methyltransferase homolog gene, partial cds. | Streptomyces caelestis | 40,260 | 07-DEC-1997 |
| | | GB_EST9:C19712 | 399 | C19712 | C19712 Rice panicle at ripening stage Oryza sativa cDNA clone E10821_1A, mRNA sequence. | Oryza sativa | 45,425 | 24-OCT-1996 |
| rx01712 | 805 | GB_EST21:AA952466 | 278 | AA952466 | TENS1404 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 1404 5', mRNA sequence | Trypanosoma cruzi | 40,876 | 29-OCT-1998 |

TABLE 4: ALIGNMENT RESULTS

| GB_EST21:AA952486 | 278 | AA952466 | TENS1404 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 1404 5', mRNA sequence. | 41,367 | 29-OCT-1998 |
|-------------------|--------|----------|--|---------|-------------|
| GB_EST21:AA952486 | 278 | AA952466 | TENS1404 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 1404 5', mRNA sequence. | 41,367 | 29-OCT-1998 |
| GB_HTG1:HSDJ534K7 | 154416 | AL109925 | Homo sapiens chromosome 1 clone RP4-534K7, *** SEQUENCING IN PROGRESS ***, in unordered pieces. | 35,651 | 23-Nov-99 |
| GB_HTG1:HSDJ534K7 | 154416 | AL109925 | Homo sapiens chromosome 1 clone RP4-534K7, *** SEQUENCING IN PROGRESS ***, in unordered pieces. | 35,651 | 23-Nov-99 |
| GB_EST27:AI447108 | 431 | AI447108 | mq91e08 x1 Siratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:586118 3', mRNA sequence. | 39,671 | 09-MAR-1999 |
| GB_PR4:AC006322 | 179640 | AC006322 | Homo sapiens PAC clone DJ1060B11 from 7q11.23-q21.1, complete sequence. | 35,817 | 18-MAR-1999 |
| GB_PL2:TM018A10 | 106184 | AF013294 | Arabidopsis thaliana BAC TM018A10. | 35,698 | 12-Jul-97 |
| GB_PR4:AC006322 | 179640 | AC006322 | Homo sapiens PAC clone DJ1060B11 from 7q11.23-q21.1, complete sequence. | 37,243 | 18-MAR-1999 |
| GB_EST3:R46227 | 443 | R46227 | yg52a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36000 3', mRNA sequence. | 42,812 | 22-MAY-1995 |
| GB_EST3:R46227 | 443 | R46227 | yg52a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36000 3', mRNA sequence. | 42,655 | 22-MAY-1995 |
| GB_BA1:MTCY190 | 34150 | Z70283 | Mycobacterium tuberculosis H37Rv complete genome; segment 98/162. | 59,294 | 17-Jun-98 |
| GB_BA1:MLCB22 | 40281 | Z98741 | Mycobacterium leprae cosmid B22. | 57,584 | 22-Aug-97 |
| GB_BA1:SC5F7 | 40024 | AL096872 | Streptomyces coelicolor cosmid 5F7. | 61,810 | 22-Jul-99 |
| GB_EST21:AA918454 | 416 | AA918454 | om38c02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1543298 3' similar to WP-F28F8.3 CED9757 SMALL NUCLEAR RIBONUCLEOPROTEIN E.; mRNA sequence. | 39,655 | 23-Jun-98 |
| GB_EST4:H34042 | 345 | H34042 | EST110563 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA clone RPNB181 5' end, mRNA sequence. | 35,942 | 2-Apr-98 |
| GB_EST20:AA899038 | 450 | AA899038 | NCP6G8T7 Perithecial Neurospora crassa cDNA clone NP6G8 3' end, mRNA sequence. | 40,000 | 12-Apr-98 |
| GB_BA1:AP000063 | 185300 | AP000063 | Aeropyrum pernix genomic DNA, section 6/7. | 40,067 | 22-Jun-99 |
| GB_HTG4:AC010694 | 115857 | AC010694 | Drosophila melanogaster clone RPC198-6H2, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces. | 35,450 | 16-OCT-1999 |
| GB_HTG4:AC010694 | 115857 | AC010694 | Drosophila melanogaster clone RPC198-6H2, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces. | 35,450 | 16-OCT-1999 |
| GB_BA1:CGL007732 | 4460 | AJ007732 | Corynebacterium glutamicum 3' ppc gene, sec3 gene, ood gene and 5' soxA gene. | 100,000 | 7-Jan-99 |
| GB_RO:RATLGL | 7601 | M24108 | Rattus norvegicus (clone A2U42) alpha2u globulin gene, exons 1-7. | 38,692 | 15-DEC-1994 |
| GB_OV:APIGY2 | 1381 | X78272 | Anas platyrhynchos (Super M) IgY upislon heavy chain gene, exon 2. | 36,962 | 15-Feb-99 |
| GB_EST30:AI629479 | 353 | AI629479 | 486101D10.x1 486 - leaf primordia cDNA library from Hake lab Zea mays cDNA, mRNA sequence. | 38,109 | 26-Apr-99 |
| GB_STS:G48245 | 515 | G48245 | SHGC-62915 Human Homo sapiens STS genomic, sequence tagged site. | 37,021 | 26-MAR-1999 |
| GB_GSS3:B49052 | 515 | B49052 | RPC11-4112.TV RPC1-11 Homo sapiens genomic clone RPC1-11-4112, genomic survey sequence. | 37,021 | 8-Apr-99 |

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TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|----------|------|-------------------|--------|----------|---|----------------------------------|---------|-------------|
| rxa01850 | 1470 | GB_BA2:ECOUW67_0 | 110000 | U18997 | Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes. | Escherichia coli | 37,196 | U18997 |
| | | GB_BA2:AE000392 | 10345 | AE000392 | Escherichia coli K-12 MG1655 section 282 of 400 of the complete genome. | Escherichia coli | 38,021 | 12-Nov-98 |
| | | GB_BA2:U32715 | 13136 | U32715 | Haemophilus influenzae Rd section 30 of 163 of the complete genome. | Haemophilus influenzae Rd | 39,860 | 29-MAY-1998 |
| rxa01878 | 1002 | GB_HTG1:CEY64F11 | 177748 | Z99776 | Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces. | Caenorhabditis elegans | 37,564 | 14-OCT-1998 |
| | | GB_HTG1:CEY64F11 | 177748 | Z99776 | Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces. | Caenorhabditis elegans | 37,564 | 14-OCT-1998 |
| | | GB_HTG1:CEY64F11 | 177748 | Z99776 | Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces. | Caenorhabditis elegans | 37,576 | 14-OCT-1998 |
| rxa01892 | 852 | GB_BA1:MTCY274 | 39991 | Z74024 | Mycobacterium tuberculosis H37Rv complete genome; segment 126/162. | Mycobacterium tuberculosis | 35,910 | 19-Jun-98 |
| | | GB_BA1:MLCB250 | 40603 | Z97369 | Mycobacterium leprae cosmid B250. | Mycobacterium leprae | 64,260 | 27-Aug-99 |
| | | GB_BA1:MSGB1529CS | 36985 | L78824 | Mycobacterium leprae cosmid B1529 DNA sequence. | Mycobacterium leprae | 64,260 | 15-Jun-96 |
| rxa01894 | 978 | GB_BA1:MTCY274 | 39991 | Z74024 | Mycobacterium tuberculosis H37Rv complete genome; segment 126/162. | Mycobacterium tuberculosis | 37,229 | 19-Jun-98 |
| | | GB_IN1:CELF46H5 | 38886 | U41543 | Caenorhabditis elegans cosmid F46H5. | Caenorhabditis elegans | 38,525 | 29-Nov-96 |
| | | GB_HTG3:AC009204 | 115633 | AC009204 | Drosophila melanogaster chromosome 2 clone BACR03E19 (D1033) RPCI-98 03.E.19 map 36E-37C strain y; on bw sp. *** SEQUENCING IN PROGRESS ***, 94 unordered pieces. | Drosophila melanogaster | 31,579 | 18-Aug-99 |
| rxa01920 | 1125 | GB_BA2:AF112536 | 1798 | AF112536 | Corynebacterium glutamicum ribonucleotide reductase beta-chain (nrdF) gene, complete cds. | Corynebacterium glutamicum | 99,733 | 5-Aug-99 |
| | | GB_BA1:CANRDFGEN | 6054 | Y09572 | Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes. | Corynebacterium ammoniagenes | 70,321 | 18-Apr-98 |
| rxa01928 | 960 | GB_BA2:AF050168 | 1228 | AF050168 | Corynebacterium ammoniagenes ribonucleoside diphosphate reductase small subunit (nrdF) gene, complete cds. | Corynebacterium ammoniagenes | 72,082 | 23-Apr-98 |
| | | GB_BA1:CGPAN | 2164 | X96580 | C. glutamicum panB, panC & xylB genes. | Corynebacterium glutamicum | 100,000 | 11-MAY-1999 |
| | | GB_PL1:AP000423 | 154478 | AP000423 | Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia. | Chloroplast Arabidopsis thaliana | 35,917 | 15-Sep-99 |
| rxa01929 | 936 | GB_BA1:CGPAN | 2164 | X96580 | C. glutamicum panB, panC & xylB genes. | Corynebacterium glutamicum | 33,925 | 15-Sep-99 |
| | | GB_BA1:XCU33548 | 8429 | U33548 | Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia. | Chloroplast Arabidopsis thaliana | 100,000 | 11-MAY-1999 |
| rxa01940 | 1059 | GB_BA1:XANHRPB6A | 1329 | M99174 | Xanthomonas campestris hrpB6 gene, complete cds. | Corynebacterium glutamicum | 38,749 | 19-Sep-96 |
| | | GB_IN2:CFU43371 | 1060 | U43371 | Critidia fasciculata inosine-uridine preferring nucleoside hydrolase (IUNH) gene, complete cds. | Xanthomonas campestris | 39,305 | 14-Sep-93 |
| rx02022 | 1230 | GB_BA2:AE001467 | 11601 | AE001467 | Helicobacter pylori strain J99 section 28 of 132 of the complete genome. | Critidia fasciculata | 61,417 | 18-Jun-96 |
| | | GB_RO:AF175967 | 3492 | AF175967 | Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds. | Helicobacter pylori J99 | 38,560 | 20-Jan-99 |
| | | GB_BA1:CGDAPE | 1966 | X81379 | C. glutamicum dapE gene and orf2. | Mus musculus | 40,275 | 26-Sep-99 |
| | | GB_BA1:CGDNAAROP | 2612 | X85965 | C. glutamicum ORF3 and aroP gene. | Corynebacterium glutamicum | 100,000 | 8-Aug-95 |
| rx02024 | 859 | GB_BA1:APU47055 | 6469 | U47055 | Anabaena PCC7120 nitrogen fixation proteins (nifE, nifN, nifX, nifW) genes, complete cds, and nitrogenase (nifK) and hesA genes, partial cds. | Corynebacterium glutamicum | 38,889 | 30-Nov-97 |
| | | GB_BA1:MTCI364 | 29540 | Z93777 | Mycobacterium tuberculosis H37Rv complete genome, segment 52/162. | Anabaena PCC7120 | 36,647 | 17-Feb-96 |
| | | | | | | Mycobacterium tuberculosis | 59,415 | 17-Jun-98 |

TABLE 4: ALIGNMENT RESULTS

| TABLE 4: ALIGNMENT REFERENCES | | | | | | | |
|-------------------------------|-------------------|--------|-------------------|---|----------------------------|--------|-------------|
| | GB_BA1:MSGB1912CS | 38503 | L01536 | M. leprae genomic dna sequence, cosmid b1912. | Mycobacterium leprae | 57,093 | 14-Jun-96 |
| | GB_BA1:MLU15180 | 38675 | U15180 | Mycobacterium leprae cosmid B1756. | Mycobacterium leprae | 57,210 | 09-MAR-1995 |
| rx02027 | | | | | | | |
| rx02031 | | | | | | | |
| rx02072 | 1464 | 2037 | X72855 | C.glutamicum GDHA gene. | Corynebacterium glutamicum | 99,317 | 24-MAY-1993 |
| | | 2037 | X59404 | Corynebacterium glutamicum, gdh gen for glutamate dehydrogenase. | Corynebacterium glutamicum | 94,367 | 30-Jul-99 |
| | | 1628 | Y18494 | Pseudomonas aeruginosa gdhA gene, strain PAC1. | Pseudomonas aeruginosa | 62,247 | 6-Feb-99 |
| rx02085 | 2358 | 22550 | Z95585 | Mycobacterium tuberculosis H37Rv complete genome; segment 49/162. | Mycobacterium tuberculosis | 38,442 | 17-Jun-98 |
| | | 42224 | Z94723 | Mycobacterium leprae cosmid B33. | Mycobacterium leprae | 56,486 | 24-Jun-97 |
| | | 91414 | M87049 | E. coli genomic sequence of the region from 84.5 to 86.5 minutes. | Escherichia coli | 52,127 | 29-MAY-1995 |
| | | 452 | AA448146 | zw82h01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE.782737 5', Homo sapiens mRNA sequence. | Homo sapiens | 34,163 | 4-Jun-97 |
| rx02093 | 927 | 444 | AA641937 | ns18b10.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1183963 5', Homo sapiens mRNA sequence. | Homo sapiens | 35,586 | 27-OCT-1997 |
| | | 143029 | AC003074 | Human PAC clone DJ0596009 from 7p15, complete sequence. | Homo sapiens | 31,917 | 6-Nov-97 |
| rx02106 | 1179 | 37620 | AL023496 | Streptomyces coelicolor cosmid 1A6. | Streptomyces coelicolor | 35,818 | 13-Jan-99 |
| | | 179651 | AC005553 | Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence. | Homo sapiens | 34,274 | 31-DEC-1998 |
| | | 397 | R49746 | yg71g10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:38768 5' similar to gb:V00567 BETA-2-MICROGLOBULIN PRECURSOR (HUMAN);. mRNA sequence. | Homo sapiens | 41,162 | 18-MAY-1995 |
| rx02111 | 1407 | 36734 | AL049497 | Streptomyces coelicolor cosmid 6G10. | Streptomyces coelicolor | 50,791 | 24-MAR-1999 |
| | | 41171 | U00010 | Mycobacterium leprae cosmid B1170. | Mycobacterium leprae | 37,563 | 01-MAR-1994 |
| | | 32437 | Z95586 | Mycobacterium tuberculosis H37Rv complete genome; segment 70/162. | Mycobacterium tuberculosis | 39,504 | 24-Jun-99 |
| rx02112 | 960 | 157658 | AC010579 | Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPCI-98 09.D.8 map 96F-96F strain y, cn bw sp, *** SEQUENCING IN PROGRESS *** | Drosophila melanogaster | 37,909 | 24-Sep-99 |
| | | 1191 | B09839 | 121 unordered pieces. T12A12-Sp6 TAMU Arabidopsis thaliana genomic clone T12A12, genomic survey sequence. | Arabidopsis thaliana | 37,843 | 14-MAY-1997 |
| | | 157658 | AC010579 | Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPCI-98 09.D.8 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** | Drosophila melanogaster | 37,909 | 24-Sep-99 |
| | | | X83011 | 121 unordered pieces. S.coelicolor secY locus DNA. | Streptomyces coelicolor | 36,533 | 02-MAR-1998 |
| rx02134 | 1044 | 6154 | GB_BA1:SCSECYDNA | BNLGH10185 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AC004005) putative ribosomal protein L7 [Arabidopsis thaliana]. mRNA sequence. | Gossypium hirsutum | 33,451 | 11-Jun-99 |
| | | 568 | GB_EST32:A1731596 | S.coelicolor secY locus DNA. | Streptomyces coelicolor | 36,756 | 02-MAR-1998 |
| | | | GB_BA1:SCSECYDNA | | | | |

TABLE 4: ALIGNMENT RESULTS

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|---------|------|-------------------|--------|----------|---|----------------------------|---------|-----------|
| rx02135 | 1197 | GB_PR3:HS525L6 | 168111 | AL023807 | Human DNA sequence from clone RP3-525L6 on chromosome 6p22.3-23 Contains CA repeat, STSs, GSSs and a CpG island, complete sequence. | Homo sapiens | 34,365 | 23-Nov-99 |
| | | GB_PL2:ATF21P8 | 85785 | AL022347 | Arabidopsis thaliana DNA chromosome 4, BAC clone F21P8 (ESSA project) | Arabidopsis thaliana | 34,325 | 9-Jun-99 |
| rx02136 | 645 | GB_PL2:U89959 | 106973 | U89959 | Arabidopsis thaliana BAC T7123, complete sequence. | Arabidopsis thaliana | 33,874 | 26-Jun-98 |
| | | GB_PL2:ATAC005819 | 57752 | AC005819 | Arabidopsis thaliana chromosome II BAC T3A4 genomic sequence, complete sequence. | Arabidopsis thaliana | 34,123 | 3-Nov-98 |
| | | GB_PL2:F15K9 | 71097 | AC005278 | Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence. | Arabidopsis thaliana | 31,260 | 7-Nov-98 |
| rx02139 | 1962 | GB_PL2:U89959 | 106973 | U89959 | Arabidopsis thaliana BAC T7123, complete sequence. | Arabidopsis thaliana | 34,281 | 26-Jun-98 |
| | | GB_BA1:MTCY190 | 34150 | Z70283 | Mycobacterium tuberculosis H37Rv complete genome; segment 98/162. | Mycobacterium tuberculosis | 62,904 | 17-Jun-98 |
| | | GB_BA1:MSG81554CS | 36548 | L78814 | Mycobacterium leprae cosmid B1554 DNA sequence. | Mycobacterium leprae | 36,648 | 15-Jun-96 |
| | | GB_BA1:MSG81551CS | 36548 | L78813 | Mycobacterium leprae cosmid B1551 DNA sequence. | Mycobacterium leprae | 36,648 | 15-Jun-96 |
| rx02153 | 903 | GB_BA2:AF049897 | 9196 | AF049897 | Corynebacterium glutamicum N-acetylglutarylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. | Corynebacterium glutamicum | 99,104 | 1-Jul-98 |
| | | GB_BA1:AF005242 | 1044 | AF005242 | Corynebacterium glutamicum N-acetylglutamate-5-semialdehyde dehydrogenase (argC) gene, complete cds. | Corynebacterium glutamicum | 99,224 | 2-Jul-97 |
| | | GB_BA1:CGARGCJBD | 4355 | X86157 | C glutamicum argC, argJ, argB, argD, and argF genes. | Corynebacterium glutamicum | 100,000 | 25-Jul-96 |
| rx02154 | 414 | GB_BA2:AF049897 | 9196 | AF049897 | Corynebacterium glutamicum N-acetylglutarylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds | Corynebacterium glutamicum | 98,551 | 1-Jul-98 |
| | | GB_BA1:AF005242 | 1044 | AF005242 | Corynebacterium glutamicum N-acetylglutamate-5-semialdehyde dehydrogenase (argC) gene, complete cds. | Corynebacterium glutamicum | 98,477 | 2-Jul-97 |
| | | GB_BA1:CGARGCJBD | 4355 | X86157 | C glutamicum argC, argJ, argB, argD, and argF genes. | Corynebacterium glutamicum | 100,000 | 25-Jul-96 |
| rx02155 | 1287 | GB_BA1:CGARGCJBD | 4355 | X86157 | C glutamicum argC, argJ, argB, argD, and argF genes. | Corynebacterium glutamicum | 99,767 | 25-Jul-96 |
| | | GB_BA2:AF049897 | 9196 | AF049897 | Corynebacterium glutamicum N-acetylglutarylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. | Corynebacterium glutamicum | 99,378 | 1-Jul-98 |
| | | GB_BA1:MSG81133CS | 42106 | L78811 | Mycobacterium leprae cosmid B1133 DNA sequence. | Mycobacterium leprae | 55,504 | 15-Jun-96 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|------------------|-------|----------|---|----------------------------|---------|-----------|
| rx02156 | 1074 | GB_BA2:AF049897 | 9196 | AF049897 | Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. C.glutamicum argC, argJ, argB, argD, and argF genes. | Corynebacterium glutamicum | 100,000 | 1-Jul-98 |
| | | GB_BA1:CGARGCJBD | 4355 | X86157 | | Corynebacterium glutamicum | 100,000 | 25-Jul-96 |
| | | GB_BA2:AE001816 | 10007 | AE001816 | Thermotoga maritima section 128 of 136 of the complete genome. | Thermotoga maritima | 50,238 | 2-Jun-99 |
| rx02157 | 1296 | GB_BA2:AF049897 | 9196 | AF049897 | Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. C.glutamicum argC, argJ, argB, argD, and argF genes. | Corynebacterium glutamicum | 99,612 | 1-Jul-98 |
| | | GB_BA1:CGARGCJBD | 4355 | X86157 | | Corynebacterium glutamicum | 99,612 | 25-Jul-96 |
| | | GB_BA1:MTCY06H11 | 38000 | Z85982 | Mycobacterium tuberculosis H37Rv complete genome; segment 73/162. | Mycobacterium tuberculosis | 57,278 | 17-Jun-98 |
| rx02158 | 1080 | GB_BA2:AF049897 | 9196 | AF049897 | Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. Corynebacterium glutamicum ornithine carbamoyltransferase (argF) gene, complete cds. | Corynebacterium glutamicum | 100,000 | 1-Jul-98 |
| | | GB_BA2:AF031518 | 2045 | AF031518 | | Corynebacterium glutamicum | 99,898 | 5-Jan-99 |
| | | GB_BA1:CGARGCJBD | 4355 | X86157 | | Corynebacterium glutamicum | 100,000 | 25-Jul-96 |
| rx02159 | 636 | GB_BA2:AF049897 | 9196 | AF049897 | Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. Corynebacterium glutamicum ornithine carbamoyltransferase (argF) gene, complete cds. | Corynebacterium glutamicum | 99,843 | 1-Jul-98 |
| | | GB_BA2:AF031518 | 2045 | AF031518 | | Corynebacterium glutamicum | 88,679 | 5-Jan-99 |
| | | GB_BA2:AF041436 | 516 | AF041436 | Corynebacterium glutamicum arginine repressor (argR) gene, complete cds. | Corynebacterium glutamicum | 100,000 | 5-Jan-99 |
| rx02160 | 1326 | GB_BA2:AF049897 | 9196 | AF049897 | Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. Corynebacterium glutamicum argininosuccinate synthetase (argG) gene, complete cds. | Corynebacterium glutamicum | 99,774 | 1-Jul-98 |
| | | GB_BA2:AF030520 | 1206 | AF030520 | | Corynebacterium glutamicum | 99,834 | 19-Nov-97 |
| | | GB_BA1:SCARGGH | 1909 | Z49111 | S.clavuligerus argG gene and argH gene (partial). | Streptomyces clavuligerus | 65,913 | 22-Apr-96 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|-------------------|--------|----------|---|-----------------------------|---------|-------------|
| rx02162 | 1554 | GB_BA2:AF049897 | 9196 | AF049897 | Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. | Corynebacterium glutamicum | 88,524 | 1-Jul-98 |
| | | GB_BA2:AF048764 | 1437 | AF048764 | Corynebacterium glutamicum argininosuccinate lyase (argH) gene, complete cds. | Corynebacterium glutamicum | 87,561 | 1-Jul-98 |
| rx02176 | 1251 | GB_BA1:MTCY06H11 | 38000 | Z85982 | Mycobacterium tuberculosis H37Rv complete genome; segment 73/162. | Mycobacterium tuberculosis | 64,732 | 17-Jun-98 |
| | | GB_BA1:MTCY31 | 37630 | Z73101 | Mycobacterium tuberculosis H37Rv complete genome; segment 41/162. | Mycobacterium tuberculosis | 36,998 | 17-Jun-98 |
| | | GB_BA1:CGGLTG | 3013 | X86112 | C glutamicum glt gene for citrate synthase and ORF. | Corynebacterium glutamicum | 39,910 | 17-Feb-95 |
| | | GB_PL2:PGU65399 | 2700 | U65399 | Basidiomycete CECT 20197 phenoloxidase (pox1) gene, complete cds. | basidiomycete CECT 20197 | 38,474 | 19-Jul-97 |
| rx02189 | 861 | GB_PR3:AC002468 | 115888 | AC002468 | Human Chromosome 15q26.1 PAC clone pDJ417d7, complete sequence. | Homo sapiens | 35,941 | 16-Sep-98 |
| | | GB_BA1:MSGB1970CS | 39399 | L78815 | Mycobacterium leprae cosmid B1970 DNA sequence. | Mycobacterium leprae | 40,286 | 15-Jun-96 |
| rx02193 | 1701 | GB_PR3:AC002468 | 115888 | AC002468 | Human Chromosome 15q26.1 PAC clone pDJ417d7, complete sequence. | Homo sapiens | 33,689 | 16-Sep-98 |
| | | GB_BA1:BRLASPA | 1987 | D25316 | Brevibacterium flavum aspA gene for aspartase, complete cds. | Corynebacterium glutamicum | 99,353 | 6-Feb-99 |
| | | GB_PAT:E04307 | 1581 | E04307 | DNA encoding Brevibacterium flavum aspartase. | Corynebacterium glutamicum | 99,367 | 29-Sep-97 |
| | | GB_BA1:ECOUW93 | 338534 | U14003 | Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes. | Escherichia coli | 37,651 | 17-Apr-96 |
| rx02194 | 966 | GB_BA2:AF050166 | 840 | AF050166 | Corynebacterium glutamicum ATP phosphoribosyltransferase (hisG) gene, complete cds. | Corynebacterium glutamicum | 98,214 | 5-Jan-99 |
| | | GB_BA1:BRLASPA | 1987 | D25316 | Brevibacterium flavum aspA gene for aspartase, complete cds. | Corynebacterium glutamicum | 93,805 | 6-Feb-99 |
| | | GB_PAT:E08649 | 188 | E08649 | DNA encoding part of aspartase from coryneform bacteria. | Corynebacterium glutamicum | 100,000 | 29-Sep-97 |
| rx02195 | 393 | GB_BA2:AF086704 | 264 | AF086704 | Corynebacterium glutamicum phosphoribosyl-ATP-pyrophosphohydrolase (hisE) gene, complete cds | Corynebacterium glutamicum | 100,000 | 8-Feb-99 |
| | | GB_BA1:EAY17145 | 6019 | Y17145 | Eubacterium acidaminophilum grdR, grdI, grdH genes and partial ldc. grdT genes. | Eubacterium acidaminophilum | 39,075 | 5-Aug-98 |
| rx02197 | 551 | GB_STS:G01195 | 332 | G01195 | fruit fly STS Dm1930 clone DS06959 T7. | Drosophila melanogaster | 35,542 | 28-Feb-95 |
| | | GB_BA1:MTCY261 | 27322 | Z97559 | Mycobacterium tuberculosis H37Rv complete genome; segment 95/162. | Mycobacterium tuberculosis | 33,938 | 17-Jun-98 |
| | | GB_BA1:MLCB2533 | 40245 | AL035310 | Mycobacterium leprae cosmid B2533. | Mycobacterium leprae | 65,517 | 27-Aug-99 |
| | | GB_BA1:U00017 | 42157 | U00017 | Mycobacterium leprae cosmid B2126. | Mycobacterium leprae | 36,770 | 01-MAR-1994 |
| rx02198 | 2599 | GB_BA1:U00017 | 42157 | U00017 | Mycobacterium leprae cosmid B2126 | Mycobacterium leprae | 38,674 | 01-MAR-1994 |
| | | GB_BA1:MLCB2533 | 40245 | AL035310 | Mycobacterium leprae cosmid B2533. | Mycobacterium leprae | 65,465 | 27-Aug-99 |
| | | GB_BA1:MTCY261 | 27322 | Z97559 | Mycobacterium tuberculosis H37Rv complete genome; segment 95/162. | Mycobacterium tuberculosis | 37,577 | 17-Jun-98 |
| rx02208 | 1025 | GB_BA1:U00017 | 42157 | U00017 | Mycobacterium leprae cosmid B2126. | Mycobacterium leprae | 59,823 | 01-MAR-1994 |
| | | GB_BA1:AP000063 | 185300 | AP000063 | Aeropyrum pernix genomic DNA, section 6/7. | Aeropyrum pernix | 39,442 | 22-Jun-99 |
| | | GB_PR4:AC06236 | 127593 | AC06236 | Homo sapiens chromosome 17, clone hCIT.162_E_12, complete sequence. | Homo sapiens | 37,191 | 29-DEC-1998 |
| rx02229 | 948 | GB_BA1:MSGY154 | 40221 | AD000002 | Mycobacterium tuberculosis sequence from clone Y154. | Mycobacterium tuberculosis | 53,541 | 03-DEC-1996 |
| | | GB_BA1:MTCY154 | 13935 | Z98209 | Mycobacterium tuberculosis H37Rv complete genome; segment 121/162. | Mycobacterium tuberculosis | 40,407 | 17-Jun-98 |
| | | GB_BA1:U00019 | 36033 | U00019 | Mycobacterium leprae cosmid B2235. | Mycobacterium leprae | 40,541 | 01-MAR-1994 |
| rx02234 | 3462 | GB_BA1:MSGB937CS | 38914 | L78820 | Mycobacterium leprae cosmid B937 DNA sequence. | Mycobacterium leprae | 66,027 | 15-Jun-96 |
| | | GB_BA1:MTCY2B12 | 20431 | Z81011 | Mycobacterium tuberculosis H37Rv complete genome; segment 61/162. | Mycobacterium tuberculosis | 71,723 | 18-Jun-98 |
| | | GB_BA2:U01072 | 4393 | U01072 | Mycobacterium bovis BCG oritidine-5'-monophosphate decarboxylase (uraA) gene. | Mycobacterium bovis | 67,101 | 22-DEC-1993 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|-------------------|--------|----------|--|-------------------------------|--------|--------------------------------|
| rx02235 | 727 | GB_BA1:MSU91572 | 960 | U91572 | Mycobacterium smegmatis carbamoyl phosphate synthetase (pyrAB) gene, partial cds and orotidine 5'-monophosphate decarboxylase (pyrF) gene, complete cds. | Mycobacterium smegmatis | 60,870 | 22-MAR-1997 |
| | | GB_HTG3:AC009364 | 192791 | AC009364 | Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 57 unordered pieces. | Homo sapiens | 37,994 | 1-Sep-99 |
| | | GB_HTG3:AC009364 | 192791 | AC009364 | Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 57 unordered pieces. | Homo sapiens | 37,994 | 1-Sep-99 |
| rx02237 | 693 | GB_BA1:MTCY21B4 | 39150 | Z80108 | Mycobacterium tuberculosis H37Rv complete genome; segment 62/162. | Mycobacterium tuberculosis | 55,844 | 23-Jun-98 |
| | | GB_BA2:AF077324 | 5228 | AF077324 | Rhodococcus equi strain 103 plasmid RE-VP1 fragment f. | Rhodococcus equi | 41,185 | 5-Nov-98 |
| | | GB_EST22:AU017763 | 586 | AU017763 | AU017763 Mouse two-cell stage embryo cDNA Mus musculus cDNA clone J074A04 3', mRNA sequence. | Mus musculus | 38,616 | 19-OCT-1998 |
| rx02239 | 1389 | GB_BA1:MTCY21B4 | 39150 | Z80108 | Mycobacterium tuberculosis H37Rv complete genome; segment 62/162. | Mycobacterium tuberculosis | 56,282 | 23-Jun-98 |
| | | GB_HTG3:AC010745 | 193862 | AC010745 | Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***, 30 unordered pieces. | Homo sapiens | 36,772 | 21-Sep-99 |
| | | GB_HTG3:AC010745 | 193862 | AC010745 | Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***, 30 unordered pieces. | Homo sapiens | 36,772 | 21-Sep-99 |
| rx02240 | 1344 | EM_PAT:E09855 | 1239 | E09855 | gDNA encoding S-adenosylmethionine synthetase. | Corynebacterium glutamicum | 99,515 | 07-OCT-1997 (Rel. 52, Created) |
| | | GB_PAT:A37831 | 5392 | A37831 | Sequence 1 from Patent WO9408014. | Streptomyces prisinaespiralis | 63,568 | 05-MAR-1997 |
| | | GB_BA2:AF117274 | 2303 | AF117274 | Streptomyces spectabilis flavoprotein homolog Dfp (dfp) gene, partial cds, and S-adenosylmethionine synthetase (metK) gene, complete cds. | Streptomyces spectabilis | 65,000 | 31-MAR-1999 |
| rx02246 | 1107 | EM_BA1:AB003693 | 5589 | AB003693 | Corynebacterium ammoniagenes DNA for rib operon, complete cds. | Corynebacterium ammoniagenes | 52,909 | 03-OCT-1997 (Rel. 52, Created) |
| | | GB_PAT:E07957 | 5589 | E07957 | gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase. | Corynebacterium ammoniagenes | 52,909 | 29-Sep-97 |
| | | GB_PAT:132742 | 5589 | 132742 | Sequence 1 from patent US 55893355. | Unknown. | 52,909 | 6-Feb-97 |
| rx02247 | 756 | GB_PAT:132743 | 2689 | 132743 | Sequence 2 from patent US 55893355. | Unknown. | 57,937 | 6-Feb-97 |
| | | EM_BA1:AB003693 | 5589 | AB003693 | Corynebacterium ammoniagenes DNA for rib operon, complete cds. | Corynebacterium ammoniagenes | 57,937 | 03-OCT-1997 (Rel. 52, Created) |
| | | GB_PAT:132742 | 5589 | 132742 | Sequence 1 from patent US 55893355. | Unknown. | 57,937 | 6-Feb-97 |
| rx02248 | 1389 | GB_PAT:132742 | 5589 | 132742 | Sequence 1 from patent US 55893355. | Unknown. | 61,843 | 6-Feb-97 |
| | | EM_BA1:AB003693 | 5589 | AB003693 | Corynebacterium ammoniagenes DNA for rib operon, complete cds. | Corynebacterium ammoniagenes | 61,843 | 03-OCT-1997 (Rel. 52, Created) |
| | | GB_PAT:E07957 | 5589 | E07957 | gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase. | Corynebacterium ammoniagenes | 61,843 | 29-Sep-97 |
| | | GB_PAT:E07957 | 5589 | E07957 | gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase. | Corynebacterium ammoniagenes | 64,346 | 29-Sep-97 |
| rx02249 | 600 | GB_PAT:132742 | 5589 | 132742 | Sequence 1 from patent US 55893355. | Unknown. | 64,346 | 6-Feb-97 |
| | | GB_PAT:132743 | 2689 | 132743 | Sequence 2 from patent US 55893355. | Unknown. | 64,346 | 6-Feb-97 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|------------------------|--------|----------|---|------------------------------|---------|--------------------------------|
| rx02250 | 643 | GB_PAT:E07957 | 5589 | E07957 | gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase. | Corynebacterium ammoniagenes | 56,318 | 29-Sep-97 |
| | | GB_PAT:I32742 | 5589 | I32742 | Sequence 1 from patent US 55893355. | Unknown. | 56,318 | 6-Feb-97 |
| | | EM_BA1:AB003693 | 5589 | AB003693 | Corynebacterium ammoniagenes DNA for rib operon, complete cds. | Corynebacterium ammoniagenes | 56,318 | 03-OCT-1997 (Rel. 52, Created) |
| rx02262 | 1269 | GB_BA1:CGL007732 | 4460 | AJ007732 | Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene | Corynebacterium glutamicum | 100,000 | 7-Jan-99 |
| | | GB_BA1:CGAMITGENE 2028 | | X93513 | C-glutamicum amt gene. | Corynebacterium glutamicum | 100,000 | 29-MAY-1996 |
| rx02263 | 488 | GB_VI:HEHCMVCG | 229354 | X17403 | Human cytomegalovirus strain AD169 complete genome. | human herpesvirus 5 | 38,651 | 10-Feb-99 |
| | | GB_BA1:CGL007732 | 4460 | AJ007732 | Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene. | Corynebacterium glutamicum | 100,000 | 7-Jan-99 |
| | | GB_BA1:CGL007732 | 4460 | AJ007732 | Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene. | Corynebacterium glutamicum | 37,526 | 7-Jan-99 |
| rx02272 | 1368 | EM_PAT:E09373 | 1591 | E09373 | Creatinine deiminase gene. | Bacillus sp. | 96,928 | 08-OCT-1997 (Rel. 52, Created) |
| | | GB_BA1:D38505 | 1591 | D38505 | Bacillus sp. gene for creatinine deaminase, complete cds. | Bacillus sp. | 96,781 | 7-Aug-98 |
| | | GB_HTG2:AC006595 | 146070 | AC006595 | Homo sapiens, *** SEQUENCING IN PROGRESS *** , 4 unordered pieces. | Homo sapiens | 36,264 | 20-Feb-99 |
| rx02281 | 1545 | GB_GSS12:AQ411010 | 551 | AQ411010 | HS_2257_B1_H02_MR CIT Approved Human Genomic Sperm Library D | Homo sapiens | 36,197 | 17-MAR-1999 |
| | | | | | Homo sapiens genomic clone Plate=2257 Col=3 Row=P, genomic survey sequence. | | | |
| | | GB_EST23:A1128623 | 363 | A1128623 | qa62c01.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1691328 3', mRNA sequence. | Homo sapiens | 37,017 | 05-OCT-1998 |
| | | GB_PL2.ATAC007019 | 102335 | AC007019 | Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence. | Arabidopsis thaliana | 33,988 | 16-MAR-1999 |
| rx02299 | 531 | GB_BA2:AF116184 | 540 | AF116184 | Corynebacterium glutamicum L-aspartate-alpha-decarboxylase precursor (panD) gene, complete cds. | Corynebacterium glutamicum | 100,000 | 02-MAY-1999 |
| | | GB_GSS9:AQ164310 | 507 | AQ164310 | HS_2171_A2_E01_MR CIT Approved Human Genomic Sperm Library D | Homo sapiens | 37,278 | 16-OCT-1998 |
| | | | | | Homo sapiens genomic clone Plate=2171 Col=2 Row=I, genomic survey sequence. | | | |
| rx02311 | 813 | GB_VI:MH68TKH | 4557 | X93468 | Murine herpesvirus type 68 thymidine kinase and glycoprotein H genes. | murine herpesvirus 68 | 40,288 | 3-Sep-96 |
| | | GB_HTG4:AC006091 | 176878 | AC006091 | Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98 | Drosophila melanogaster | 36,454 | 27-OCT-1999 |
| | | | | | 48.G.5 map 91F1-91F13 strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** , 4 unordered pieces | | | |
| | | GB_HTG4:AC006091 | 176878 | AC006091 | Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98 | Drosophila melanogaster | 36,454 | 27-OCT-1999 |
| | | | | | 48.G.5 map 91F1-91F13 strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** , 4 unordered pieces. | | | |

TABLE 4: ALIGNMENT RESULTS

| | GB_BA2:RRU65510 | 16259 | U65510 | Rhodospirillum rubrum CO-induced hydrogenase operon (cooM, cooK, cooL, cooX, cooJ, cooH) genes, iron sulfur protein (cooF) gene, carbon monoxide dehydrogenase (cooS) gene, carbon monoxide dehydrogenase accessory proteins (cooC, cooT, cooJ) genes, putative transcriptional activator (cooA) gene, nicotinate-nucleotide pyrophosphorylase (nadC) gene, complete cds, L-aspartate oxidase (nadB) gene, and alkyl hydroperoxide reductase (ahpC) gene, partial cds. | Rhodospirillum rubrum | 37,828 | 9-Apr-97 |
|----------|-----------------|--------|----------|--|------------------------------|--------|-------------|
| rxa02315 | 1752 | 40051 | AD000004 | Mycobacterium tuberculosis sequence from clone y224. | Mycobacterium tuberculosis | 49,418 | 03-DEC-1996 |
| | | 40838 | Z95558 | Mycobacterium tuberculosis H37Rv complete genome; segment 28/162. | Mycobacterium tuberculosis | 49,360 | 17-Jun-98 |
| | | 40051 | AD000004 | Mycobacterium tuberculosis sequence from clone y224. | Mycobacterium tuberculosis | 38,150 | 03-DEC-1996 |
| rx02318 | 402 | 111083 | AC011348 | Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces. | Homo sapiens | 35,821 | 06-OCT-1999 |
| | | 111083 | AC011348 | Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces. | Homo sapiens | 35,821 | 06-OCT-1999 |
| | | 89234 | AC011412 | Homo sapiens chromosome 5 clone CIT978SKB_81K21, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces. | Homo sapiens | 36,181 | 06-OCT-1999 |
| rx02319 | 1080 | 40051 | AD000004 | Mycobacterium tuberculosis sequence from clone y224. | Mycobacterium tuberculosis | 37,792 | 03-DEC-1996 |
| | | 40838 | Z95558 | Mycobacterium tuberculosis H37Rv complete genome; segment 28/162. | Mycobacterium tuberculosis | 37,792 | 17-Jun-98 |
| | | 476 | A1117213 | ub83h02.r1 Soares 2NbMT Mus musculus cDNA clone IMAGE:1395123 5' mRNA sequence. | Mus musculus | 35,084 | 2-Sep-98 |
| rx02345 | 1320 | 2582 | X91189 | B.ammoniaenes purK and purE genes. | Corynebacterium ammoniagenes | 61,731 | 14-Jan-97 |
| | | 42729 | Z92771 | Mycobacterium tuberculosis H37Rv complete genome; segment 141/162. | Mycobacterium tuberculosis | 39,624 | 10-Feb-99 |
| | | 42729 | Z92771 | Mycobacterium tuberculosis H37Rv complete genome; segment 141/162. | Mycobacterium tuberculosis | 39,847 | 10-Feb-99 |
| rx02350 | 618 | 2582 | X91189 | B.ammoniaenes purK and purE genes. | Corynebacterium ammoniagenes | 64,286 | 14-Jan-97 |
| | | 129528 | X94335 | S.cerevisiae 130kb DNA fragment from chromosome XV. | Saccharomyces cerevisiae | 36,617 | 15-Jul-97 |
| | | 50984 | X90518 | S.cerevisiae DNA of 51 Kb from chromosome XV right arm. | Saccharomyces cerevisiae | 36,617 | 1-Nov-95 |
| rx02373 | 1038 | 1853 | E00311 | DNA coding of 2,5-diketogluconic acid reductase. | unidentified | 56,123 | 29-Sep-97 |
| | | 1853 | I06030 | Sequence 4 from Patent EP 0305608. | Unknown. | 56,220 | 02-DEC-1993 |
| | | 1853 | I00836 | Sequence 1 from Patent US 4758514. | Unknown. | 56,220 | 21-MAY-1993 |
| rx02375 | 1350 | 3005 | U31230 | Corynebacterium glutamicum Obg protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unkdh) gene, complete cds. | Corynebacterium glutamicum | 99,332 | 2-Aug-96 |
| | | 169072 | AC009946 | Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces. | Homo sapiens | 36,115 | 8-Sep-99 |
| | | 169072 | AC009946 | Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces. | Homo sapiens | 36,115 | 8-Sep-99 |
| rx02380 | 777 | 41230 | Z81368 | Mycobacterium tuberculosis H37Rv complete genome; segment 106/162. | Mycobacterium tuberculosis | 38,088 | 17-Jun-98 |
| | | 120754 | AC010658 | Drosophila melanogaster chromosome 3L/75C1 clone RPC198-3B20, *** SEQUENCING IN PROGRESS ***, 78 unordered pieces. | Drosophila melanogaster | 35,817 | 16-OCT-1999 |
| | | 120754 | AC010658 | Drosophila melanogaster chromosome 3L/75C1 clone RPC198-3B20, *** SEQUENCING IN PROGRESS ***, 78 unordered pieces. | Drosophila melanogaster | 35,817 | 16-OCT-1999 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|-------------------|--------|----------|---|----------------------------|---------|-------------|
| rx02382 | 1419 | GB_BA1:CGPROAGEN | 1783 | X82929 | C.glutamicum proA gene. | Corynebacterium glutamicum | 98,802 | 23-Jan-97 |
| | | GB_BA1:MTCY428 | 26914 | Z81451 | Mycobacterium tuberculosis H37Rv complete genome; segment 107/162. | Mycobacterium tuberculosis | 38,054 | 17-Jun-98 |
| | | GB_BA2:CGU31230 | 3005 | U31230 | Corynebacterium glutamicum Obg protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unkdth) gene, complete cds. | Corynebacterium glutamicum | 98,529 | 2-Aug-96 |
| rx02400 | 693 | GB_BA1:CGACEA | 2427 | X75504 | C.glutamicum aceA gene and thiX genes (partial). | Corynebacterium glutamicum | 100,000 | 9-Sep-94 |
| | | GB_PAT:186191 | 2135 | I86191 | Sequence 3 from patent US 5700661. | Unknown. | 100,000 | 10-Jun-98 |
| | | GB_PAT:113693 | 2135 | I13693 | Sequence 3 from patent US 5439822. | Unknown. | 100,000 | 26-Sep-95 |
| rx02432 | 1098 | GB_GSS15:AQ606842 | 574 | AQ606842 | HS_5404_B2_E07_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=980 Col=14 Row=J, genomic survey sequence. | Homo sapiens | 39,716 | 10-Jun-99 |
| | | GB_EST1:T05804 | 406 | T05804 | EST03693 Fetal brain, Stragatene (cat#936206) Homo sapiens cDNA clone HFBG363 similar to EST containing Alu repeat, mRNA sequence. | Homo sapiens | 37,915 | 30-Jun-93 |
| | | GB_PL1:AB006699 | 77363 | AB006699 | Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence. | Arabidopsis thaliana | 35,526 | 20-Nov-99 |
| rx02458 | 1413 | GB_BA2:AF114233 | 1852 | AF114233 | Corynebacterium glutamicum 5-enolpyruvylshikimate 3-phosphate synthase (aroA) gene, complete cds | Corynebacterium glutamicum | 100,000 | 7-Feb-99 |
| | | GB_EST37:AW013061 | 578 | AW013061 | ODT-0033 Winter flounder ovary Pleuronectes americanus cDNA clone ODT-0033 5' similar to FRUCTOSE-BISPHOSPHATE ALDOLASE B (LIVER), mRNA sequence. | Pleuronectes americanus | 39,175 | 10-Sep-99 |
| | | GB_GSS15:AQ650027 | 728 | AQ650027 | Sheared DNA-5L2.TF Sheared DNA Trypanosoma brucei genomic clone | Trypanosoma brucei | 39,281 | 22-Jun-99 |
| rx02469 | 1554 | GB_BA1:MTCY359 | 36021 | Z83859 | Sheared DNA-5L2, genomic survey sequence. | Mycobacterium tuberculosis | 39,634 | 17-Jun-98 |
| | | GB_BA1:MLCB1788 | 39228 | AL008609 | Mycobacterium tuberculosis H37Rv complete genome; segment 84/162. | Mycobacterium leprae | 59,343 | 27-Aug-99 |
| | | GB_BA1:SCAJ10601 | 4692 | AJ010601 | Mycobacterium leprae cosmid B1798. | Streptomyces coelicolor | 48,899 | 17-Sep-98 |
| rx02497 | 1050 | GB_BA2:CGU31224 | 422 | U31224 | Streptomyces coelicolor A3(2) DNA for whiD and whiK loci. | Corynebacterium glutamicum | 96,445 | 2-Aug-96 |
| | | GB_BA1:MTCY20G9 | 37218 | Z77162 | Corynebacterium glutamicum (ppx) gene, partial cds. | Mycobacterium tuberculosis | 59,429 | 17-Jun-98 |
| | | GB_BA1:SCE7 | 16911 | AL049819 | Mycobacterium tuberculosis H37Rv complete genome; segment 25/162. | Streptomyces coelicolor | 39,510 | 10-MAY-1999 |
| rx02499 | 933 | GB_BA2:CGU31225 | 1817 | U31225 | Streptomyces coelicolor cosmid E7. | Corynebacterium glutamicum | 97,749 | 2-Aug-96 |
| | | GB_BA1:NG17PILA | 1920 | X13965 | Corynebacterium glutamicum L-proline:NADP+ 5-oxidoeductase (proC) gene, complete cds. | Neisseria gonorrhoeae | 43,249 | 30-Sep-93 |
| | | GB_HTG2:AC007984 | 129715 | AC007984 | Neisseria gonorrhoeae pilA gene. | Drosophila melanogaster | 33,406 | 2-Aug-99 |
| | | | | | O5.C.10 map 97D-97E strain y; cn bw sp. *** SEQUENCING IN PROGRESS | | | |
| | | | | | ***, 87 unordered pieces. | | | |
| rx02501 | 1188 | GB_BA1:MTCY20G9 | 37218 | Z77162 | Mycobacterium tuberculosis H37Rv complete genome; segment 25/162. | Mycobacterium tuberculosis | 39,357 | 17-Jun-98 |
| | | GB_BA1:U00018 | 42991 | U00018 | Mycobacterium leprae cosmid B2168. | Mycobacterium leprae | 51,768 | 01-MAR-1994 |
| | | GB_VI:HE1CG | 152261 | X14112 | Herpes simplex virus (HSV) type 1 complete genome. | human herpesvirus 1 | 39,378 | 17-Apr-97 |
| rx02503 | 522 | GB_PR3:AC005328 | 35414 | AC005328 | Homo sapiens chromosome 19, cosmid R26660, complete sequence. | Homo sapiens | 39,922 | 28-Jul-98 |
| | | GB_PR3:AC005545 | 43514 | AC005545 | Homo sapiens chromosome 19, cosmid R26634, complete sequence. | Homo sapiens | 39,922 | 3-Sep-98 |
| | | GB_PR3:AC005328 | 35414 | AC005328 | Homo sapiens chromosome 19, cosmid R26660, complete sequence. | Homo sapiens | 34,911 | 28-Jul-98 |
| rx02504 | 681 | GB_BA1:MTCY20G9 | 37218 | Z77162 | Mycobacterium tuberculosis H37Rv complete genome; segment 25/162. | Mycobacterium tuberculosis | 54,940 | 17-Jun-98 |
| | | GB_PR3:AC005328 | 35414 | AC005328 | Homo sapiens chromosome 19, cosmid R26660, complete sequence. | Homo sapiens | 41,265 | 28-Jul-98 |
| | | GB_PR3:AC005545 | 43514 | AC005545 | Homo sapiens chromosome 19, cosmid R26634, complete sequence. | Homo sapiens | 41,265 | 3-Sep-98 |
| rx02516 | 1386 | GB_BA1:MLCL536 | 36224 | Z99125 | Mycobacterium leprae cosmid L536. | Mycobacterium leprae | 37,723 | 04-DEC-1998 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|-------------------|--------|----------|---|------------------------------------|--------|-------------|
| rx02517 | 570 | GB_BA1:U00013 | 35881 | U00013 | Mycobacterium leprae cosmid B1496. | Mycobacterium leprae | 37,723 | 01-MAR-1994 |
| | | GB_BA1:MTV007 | 32806 | AL021184 | Mycobacterium tuberculosis H37Rv complete genome; segment 64/162. | Mycobacterium tuberculosis | 61,335 | 17-Jun-98 |
| | | GB_BA1:MLCL536 | 36224 | Z99125 | Mycobacterium leprae cosmid L536. | Mycobacterium leprae | 37,018 | 04-DEC-1998 |
| | | GB_BA1:U00013 | 35881 | U00013 | Mycobacterium leprae cosmid B1496. | Mycobacterium leprae | 37,018 | 01-MAR-1994 |
| | | GB_BA1:SCC22 | 22115 | AL096839 | Streptomyces coelicolor cosmid C22. | Streptomyces coelicolor | 37,071 | 12-Jul-99 |
| rx02532 | 1170 | GB_OV:AF137219 | 831 | AF137219 | Amia calva mixed lineage leukemia-like protein (MIL) gene, partial cds. | Amia calva | 36,853 | 7-Sep-99 |
| | | GB_EST30:AI645057 | 301 | AI645057 | vs52a10.y1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence | Mus musculus | 41,860 | 29-Apr-99 |
| rx02536 | 879 | GB_EST20:AA822595 | 429 | AA822595 | vs52a10.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence. | Mus musculus | 42,353 | 17-Feb-98 |
| | | GB_HTG2:AF130866 | 118874 | AF130866 | Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS ***; in unordered pieces. | Homo sapiens | 40,754 | 21-MAR-1999 |
| | | GB_HTG2:AF130866 | 118874 | AF130866 | Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS ***; in unordered pieces. | Homo sapiens | 40,754 | 21-MAR-1999 |
| rx02550 | 1434 | GB_PL1:ATT12J5 | 84499 | AL035522 | Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 (ESSAI project). | Arabidopsis thaliana | 35,063 | 24-Feb-99 |
| | | GB_BA1:MTCY279 | 9150 | Z97991 | Mycobacterium tuberculosis H37Rv complete genome; segment 17/162. | Mycobacterium tuberculosis | 37,773 | 17-Jun-98 |
| | | GB_BA1:MSGB1970CS | 39399 | L78815 | Mycobacterium leprae cosmid B1970 DNA sequence. | Mycobacterium leprae | 39,024 | 15-Jun-96 |
| rx02559 | 1026 | GB_BA2:SC2H4 | 25970 | AL031514 | Streptomyces coelicolor cosmid 2H4. | Streptomyces coelicolor A3(2) | 37,906 | 19-OCT-1999 |
| | | GB_BA1:MTV004 | 69350 | AL009198 | Mycobacterium tuberculosis H37Rv complete genome; segment 144/162. | Mycobacterium tuberculosis | 47,358 | 18-Jun-98 |
| | | GB_PAT:I28684 | 5100 | I28684 | Sequence 1 from patent US 5573915. | Unknown. | 39,138 | 6-Feb-97 |
| rx02622 | 1683 | GB_BA1:MTU27357 | 5100 | U27357 | Mycobacterium tuberculosis cyclopropane mycolic acid synthase (cma1) gene, complete cds. | Mycobacterium tuberculosis | 39,138 | 26-Sep-95 |
| | | GB_BA2:AE001780 | 11997 | AE001780 | Thermotoga maritima section 92 of 136 of the complete genome. | Thermotoga maritima | 44,914 | 2-Jun-99 |
| | | GB_OV:AF064564 | 49254 | AF064564 | Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds. | Fugu rubripes | 39,732 | 17-Aug-99 |
| rx02623 | 714 | GB_OV:AF064564 | 49254 | AF064564 | Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds. | Fugu rubripes | 36,703 | 17-Aug-99 |
| | | GB_GSS5:AQ818728 | 444 | AQ818728 | HS_5268_A1_G09_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=844 Col=17 Row=M, genomic survey sequence. | Homo sapiens | 38,801 | 26-Aug-99 |
| | | GB_HTG5:AC011083 | 198586 | AC011083 | Homo sapiens chromosome 9 clone RP11-111M7 map 9, WORKING DRAFT SEQUENCE, 51 unordered pieces. | Homo sapiens | 35,714 | 19-Nov-99 |
| rx02629 | 708 | GB_GSS6:AQ826948 | 544 | AQ826948 | HS_5014_A2_C12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=590 Col=24 Row=E, genomic survey sequence. | Homo sapiens | 39,146 | 27-Aug-99 |
| | | GB_VI:BRSMGP | 462 | M86652 | Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds. | Bovine respiratory syncytial virus | 37,013 | 28-Apr-93 |
| | | GB_VI:BRSMGP | 462 | M86652 | Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds. | Bovine respiratory syncytial virus | 37,013 | 28-Apr-93 |

TABLE 4: ALIGNMENT RESULTS

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|---------|------|-------------------|--------|----------|---|----------------------------|--------|-------------|
| rx02645 | 1953 | GB_PAT:A45577 | 1925 | A45577 | Sequence 1 from Patent WO9519442. | Corynebacterium glutamicum | 39,130 | 07-MAR-1997 |
| | | GB_PAT:A45581 | 1925 | A45581 | Sequence 5 from Patent WO9519442. | Corynebacterium glutamicum | 39,130 | 07-MAR-1997 |
| | | GB_BA1:CORILVA | 1925 | L01508 | Corynebacterium glutamicum threonine dehydratase (ilvA) gene, complete cds. | Corynebacterium glutamicum | 39,130 | 26-Apr-93 |
| rx02646 | 1392 | GB_BA1:CORILVA | 1925 | L01508 | Corynebacterium glutamicum threonine dehydratase (ilvA) gene, complete cds. | Corynebacterium glutamicum | 99,138 | 26-Apr-93 |
| | | GB_PAT:A45585 | 1925 | A45585 | Sequence 9 from Patent WO9519442. | Corynebacterium glutamicum | 99,066 | 07-MAR-1997 |
| | | GB_PAT:A45583 | 1925 | A45583 | Sequence 7 from Patent WO9519442. | Corynebacterium glutamicum | 99,066 | 07-MAR-1997 |
| rx02648 | 1326 | GB_OV:ICTCNC | 2049 | M83111 | Ictalurus punctatus cyclic nucleotide-gated channel RNA sequence. | Ictalurus punctatus | 38,402 | 24-MAY-1993 |
| | | GB_EST11:AA265464 | 345 | AA265464 | mx91c06.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:693706 5', mRNA sequence. | Mus musculus | 38,655 | 20-MAR-1997 |
| rx02653 | | GB_GSS8:AQ006950 | 480 | AQ006950 | CIT-HSP-2294E14. TR CIT-HSP Homo sapiens genomic clone 2294E14, genomic survey sequence. | Homo sapiens | 36,074 | 27-Jun-98 |
| rx02687 | 1068 | GB_BA1:CORPHEA | 1088 | M13774 | C.glutamicum pheA gene encoding prephenate dehydratase, complete cds. | Corynebacterium glutamicum | 99,715 | 26-Apr-93 |
| | | GB_PAT:E04483 | 948 | E04483 | DNA encoding prephenate dehydratase. | Corynebacterium glutamicum | 98,523 | 29-Sep-97 |
| | | GB_PAT:E06110 | 948 | E06110 | DNA encoding prephenate dehydratase. | Corynebacterium glutamicum | 98,523 | 29-Sep-97 |
| rx02717 | 1005 | GB_PL1:HVC4H | 59748 | Y14573 | Hordeum vulgare DNA for chromosome 4H. | Hordeum vulgare | 36,593 | 25-MAR-1999 |
| | | GB_PR2:HS310H5 | 29718 | Z69705 | Human DNA sequence from cosmid 310H5 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains EST and CpG island. | Homo sapiens | 36,089 | 22-Nov-99 |
| | | GB_PR3:AC004754 | 39188 | AC004754 | Homo sapiens chromosome 16, cosmid clone RT286 (LANL), complete sequence. | Homo sapiens | 36,089 | 28-MAY-1998 |
| rx02754 | 1461 | GB_HTG2:AC008223 | 130212 | AC008223 | Drosophila melanogaster chromosome 3 clone BACR16118 (D815) RPCI-98 16.1.18 map 95A-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces. | Drosophila melanogaster | 32,757 | 2-Aug-99 |
| | | GB_HTG2:AC008223 | 130212 | AC008223 | Drosophila melanogaster chromosome 3 clone BACR16118 (D815) RPCI-98 16.1.18 map 95A-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 101 unordered pieces. | Drosophila melanogaster | 32,757 | 2-Aug-99 |
| rx02758 | 1422 | GB_BA1:MTCY71 | 42729 | Z92771 | Mycobacterium tuberculosis H37Rv complete genome; segment 1411/162. | Mycobacterium tuberculosis | 37,838 | 10-Feb-99 |
| | | GB_HTG5:AC011678 | 171967 | AC011678 | Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS *** , 20 unordered pieces. | Homo sapiens | 35,331 | 5-Nov-99 |
| | | GB_HTG5:AC011678 | 171967 | AC011678 | Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS *** , 20 unordered pieces. | Homo sapiens | 33,807 | 5-Nov-99 |
| | | GB_BA2:AF064070 | 23183 | AF064070 | Burkholderia pseudomallei putative dihydroorotase (pyrC) gene, partial cds; putative 1-acyl-sn-glycerol-3-phosphate acyltransferase (plsC), putative diadenosine tetraphosphatase (apaH), complete cds; type II O-antigen biosynthesis gene cluster, complete sequence; putative undecaprenyl phosphate N-acetylglucosaminyltransferase, and putative UDP-glucose 4-epimerase genes, complete cds; and putative galactosyl transferase gene, partial cds. | Burkholderia pseudomallei | 36,929 | 20-Jan-99 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|----------|------|-------------------|--------|----------|---|----------------------------|---------|-------------|
| rx02771 | 678 | GB_BA2:AF038651 | 4077 | AF038651 | Corynebacterium glutamicum dipeptide-binding protein (dciAE) gene, partial cds; adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds; and unknown gene. | Corynebacterium glutamicum | 99,852 | 14-Sep-98 |
| | | GB_IN1:CELT19B4 | 37121 | U80438 | Caenorhabditis elegans cosmid T19B4. | Caenorhabditis elegans | 43,836 | 04-DEC-1996 |
| | | GB_EST36:AV193572 | 360 | AV193572 | AV193572 Yuji Kohara unpublished cDNA: Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk618h8 5', mRNA sequence. | Caenorhabditis elegans | 48,588 | 22-Jul-99 |
| rx02772 | 1158 | GB_BA2:AF038651 | 4077 | AF038651 | Corynebacterium glutamicum dipeptide-binding protein (dciAE) gene, partial cds; adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds; and unknown gene. | Corynebacterium glutamicum | 99,914 | 14-Sep-98 |
| | | GB_BA1:MTCY227 | 35946 | Z77724 | Mycobacterium tuberculosis H37Rv complete genome; segment 114/162. | Mycobacterium tuberculosis | 38,339 | 17-Jun-98 |
| | | GB_BA1:U00011 | 40429 | U00011 | Mycobacterium leprae cosmid B1177. | Mycobacterium leprae | 38,996 | 01-MAR-1994 |
| rx02790 | 1266 | GB_BA1:MTCY159 | 33818 | Z83863 | Mycobacterium tuberculosis H37Rv complete genome; segment 111/162. | Mycobacterium tuberculosis | 37,640 | 17-Jun-98 |
| | | GB_PR4:AC006581 | 172931 | AC006581 | Homo sapiens 12p21 BAC RPC111-259018 (Roswell Park Cancer Institute Human BAC Library) complete sequence. | Homo sapiens | 37,906 | 3-Jun-99 |
| | | GB_PR4:AC006581 | 172931 | AC006581 | Homo sapiens 12p21 BAC RPC111-259018 (Roswell Park Cancer Institute Human BAC Library) complete sequence. | Homo sapiens | 35,280 | 3-Jun-99 |
| rx02791 | 951 | GB_BA1:MTCY159 | 33818 | Z83863 | Mycobacterium tuberculosis H37Rv complete genome; segment 111/162. | Mycobacterium tuberculosis | 39,765 | 17-Jun-98 |
| | | GB_OV:CHKCEK2 | 3694 | M35195 | Chicken tyrosine kinase (cek2) mRNA, complete cds. | Gallus gallus | 38,937 | 28-Apr-93 |
| | | GB_BA1:MSASDASK | 5037 | Z17372 | M. smegmatis asd, ask-alpha, and ask-beta genes. | Mycobacterium smegmatis | 38,495 | 9-Aug-94 |
| rx02802 | 1194 | GB_EST24:A1223401 | 169 | A1223401 | qq48g01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838448 3' similar to WP:C25D7.8 CE08394 ; mRNA sequence. | Homo sapiens | 40,828 | 27-OCT-1998 |
| | | GB_EST24:A1223401 | 169 | A1223401 | qq48g01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838448 3' similar to WP:C25D7.8 CE08394 ; mRNA sequence. | Homo sapiens | 40,828 | 27-OCT-1998 |
| rx02814 | 494 | GB_BA1:MTCY7D11 | 22070 | Z95120 | Mycobacterium tuberculosis H37Rv complete genome; segment 138/162. | Mycobacterium tuberculosis | 58,418 | 17-Jun-98 |
| | | GB_BA1:MTCY7D11 | 22070 | Z95120 | Mycobacterium tuberculosis H37Rv complete genome; segment 138/162. | Mycobacterium tuberculosis | 40,496 | 17-Jun-98 |
| | | GB_PR1:HSAJ2962 | 778 | AJ002962 | Homo sapiens mRNA for hB-FABP. | Homo sapiens | 39,826 | 8-Jan-98 |
| rx02843 | 608 | GB_BA1:CGAJ4934 | 1160 | AJ004934 | Corynebacterium glutamicum dapD gene, complete CDS. | Corynebacterium glutamicum | 100,000 | 17-Jun-98 |
| | | GB_BA1:MTCI364 | 29540 | Z93777 | Mycobacterium tuberculosis H37Rv complete genome; segment 52/162. | Mycobacterium tuberculosis | 37,710 | 17-Jun-98 |
| | | GB_BA1:MLU15180 | 38675 | U15180 | Mycobacterium leprae cosmid B1756. | Mycobacterium leprae | 39,626 | 09-MAR-1995 |
| rxs03205 | 963 | GB_BA1:BLSIGBGN | 2906 | Z49824 | Blactofermentum orf1 gene and sigB gene. | Corynebacterium glutamicum | 98,854 | 25-Apr-96 |
| | | GB_EST21:AA980237 | 377 | AA980237 | ua32a12.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1348414 5' similar to TR:Q61025 Q61025 HYPOTHETICAL 15.2 KD PROTEIN. ; mRNA sequence. | Mus musculus | 41,489 | 27-MAY-1998 |
| | | GB_EST23:A1158316 | 371 | A1158316 | ud27c05.r1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1447112 5' mRNA sequence. | Mus musculus | 38,005 | 30-Sep-98 |
| rxs03223 | 1237 | GB_IN1:LMFL2743 | 38368 | AL031910 | Leishmania major Friedlin chromosome 4 cosmid L2743. | Leishmania major | 39,869 | 15-DEC-1999 |
| | | GB_PR3:HSDJ61B2 | 119666 | AL096710 | Human DNA sequence from clone RP1-61B2 on chromosome 6p11.2-12.3 Contains isoforms 1 and 3 of BPAG1 (bullous pemphigoid antigen 1 (230/240kD), an exon of a gene similar to murine MACF cytoskeletal protein, STSs and GSSs, complete sequence. | Homo sapiens | 34,930 | 17-DEC-1999 |

TABLE 4: ALIGNMENT RESULTS

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|-----------------|--------|----------|--|--------------|--------|-------------|
| GB_PR3:HSDJ61B2 | 119666 | AL096710 | Human DNA sequence from clone RP1-61B2 on chromosome 6p11.2-12.3 Contains isoforms 1 and 3 of BPAG1 (bullous pemphigoid antigen 1 (230/240kD), an exon of a gene similar to murine MACF cytoskeletal protein, STGs and GSSs, complete sequence. | Homo sapiens | 34,634 | 17-DEC-1999 |
|-----------------|--------|----------|--|--------------|--------|-------------|